Example 1; SEQ ID NO 19298; 1481pp; English.

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the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomytalitis), uvaitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention of and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by charmed immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 KGELAMRNIEARGLKOMKRQGDANVKGE-EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 AGEL------GINYVKIDGNVGVIGNGAGLVMSTL--------DCVAYAGENF 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKITEEINKAI----DDAIAAIEQSETID----PMKVPDHADKFERHVGIVD-----F 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTHVISDIODFVVALSLEISDEG-NITMTSFEVROFANVVNHIGGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes predicted ORF-encoded polypeptide #19298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.9%; Score 84.5; DB 4; Length 436; 26.0%; Pred. No. 4.5; cive 20; Mismatches 61; Indels 4'
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABM54622 standard; protein; 436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2002; 2002WO-US032727.
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Zhang Y, Wang S, Jen S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity ?
....hes 45; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 436 AA;
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The invention relates to an isolated polymucleotide (Attrea4357-Acre4753) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to imminogenic fragments of P. acnes polypeptides. The invention and to imminogenic fragments of P. acnes polypeptides of the invention additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising of the invention; used to be invention; and the invention; and polymention from the comprising of the invention; a method for stimulating an immune response specific for a P. acnes to polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition proteins, T cell populations, or confidence of the invention; or for detecting or determining the development of P. acnes in a carison presenting cells that express the polymedicties, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in correcting, T cell populations or antigen-presenting cells that express the polymeties are useful for diagnosing, preventing or treating acnes to protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes polymetic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymetice of and diagnostic candid to be encoded by an ORF (open canding frame) contained within the P. acnes polymetices of the cinnend within the P. acnes polymetices of the printed specification, but was obtained in electronic format directly from Interface of the pri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 DATLVEVNPMIKTGDGRILAIDGKWTVDNNASFRQPDHA-----GLVDRATTDPLELR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 KGELAMRNIEARGLKOMKROGDANVKGE-EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283 AGEL-----GLNYVKLDGNVGVIGNGAGLVMSTL-------DCVAYAGENF 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                          invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 DKITERINKAI---DDAIAAIEQSETID---PMKVPDHADKFERHVGIVD------F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 PITHVISDIQDFVVALSLEISDEG-NITMISFEVROFANVVNHIGGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 PGSPAPANFLDIGGGASAEIMANGLDLIMSDEQVRSV--FVNVFGGITACDQV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;

    epidermidis open reading frame protein sequence SEQ ID NO:50.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 84.5; Di
26.0%; Pred. No. 4.5;
tive 20; Mismatches
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Best Local Similarity
Matches 45; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 436 AA;
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Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
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                                                     Claim 18; Page 59; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001 (first entry)
                                                                                                                                                                         for SEQ ID NO:4455 to 4464
                     WPI; 2001-316495/33
                         N-PSDB; AAH52328
                                                                                                                                                                                    Sequence 817 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                            endocarditis.
          Kimmerly WJ;
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Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                      Claim 18; Page 432; 2188pp; English.
                09-NOV-2000; 2000WO-US030782
                                  99US-0164258P
                                                   (GLAX ) GLAXO GROUP LTD
                                                                                    WPI; 2001-316495/33.
N-PSDB; AAH53067.
                                                                                                                                                                                                                                                                                                                                            Sequence 817 AA;
                                  199-NOV-1999;
                                                                    Kimmerly WJ;
17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                          504 DILHKRVIGQNDAVNSİSKAVRRARAĞLK----DP-----KRPIĞSFIFLĞPTG 548
                                                                                                                                                                                                                                                                                                                                                                                                                KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                             72
                                                                                                                                                                                                                                                                                                                                                                                         549 VGKTELARALAESMFGEDDAMIRVDMSEFWEXHAVSRLVGAPPGYVGHDDGGQLTEKVRR
                                                                                                                                                                                                                                                                                                                                            18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                            87; Indels 45; Gaps
                                                             Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                           DB 4; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 ELODORFAGFGGASEGSDYETVRKTMMKELKNSFRPE 700
                                                                                                                                                                                                                                                                                                          Ouery Match
7.9%; Score 84.5; Di
Best Local Similarity 23.0%; Pred. No. 11;
Matches 50; Conservative 35; Mismatches
  (GLAX ) GLAXO GROUP LTD
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11;
                                                                                          548
                                                                                                                                      549 VGKTELARALAESMFGEDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                                                                                                                                                         121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMISFEVROFANVV----NHIGGL 172
                                                                                                                                                                                          73 MRNIE-ARGL-KOMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY
                                                                DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
          DB 4; Length 817;
                                     Indels
                                                                                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDIVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                   664 ELQDQRFAGFGGASBGSDYETVRKTMMKELKNSFRPE 700
                                     87;
           7.9%; Score 84.5; Di
23.0%; Pred. No. 11;
Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                               ABU43148 standard; protein; 817 AA.
Query Match
Best Local Similarity 23...
Best Local Similarity
Local S0; Conservative
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Antisense; prokaryotic essential gene; cell proliferation; drug design.

Protein encoded by Prokaryotic essential gene #28675.

(first entry)

19-JUN-2003

ABU43148;

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the inventor tradec's to an inventor acts compitably any one of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the cartisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a blological pathway crequired for proliferation, or that inhibits proliferation or the biological dentifying a gene product or that has an activity against a blological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene or organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene or to which each of the strains is present in a culture or collection of the strains or strains; or (3) identifying the target of a compound that inhibits the collection of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologus mucleic acids required for cellular promoter minder acids are useful for confident and all an enganged or antidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRNIE-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                      Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 11; 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID NO 71072; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                    Malone C,
Carr GJ,
                                                                                                                                                                                                                          06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-034293P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                          21-MAR-2002; 2002WO-US009107
                          Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003-029926/02
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N-PSDB; ACA47018
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                                                                    WO200277183-A2
                                                                                                                                                                                                    21-MAR-2001;
                                                                                                               03-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                 Wang L,
Wall D,
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Matches
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to soreen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
549 VGKTELARALAESMFGEDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                                         609 K----PYSVILFDBIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTVIMTSNVGAO 663
                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :| :| :| | :| | :
510 DTLHKRVIGQNDAVNSISKAVRRARAGLK-----DP-------KRPIGSFIFLGPTG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 DPIH----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                                121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
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                                                                                                   173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.9%; Score 84.5; D
23.0%; Pred. No. 11;
Live 35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                      ABP39236 standard; protein; 823
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97US-0064964P.
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                                                                                                                                                                                                                                                                                                                                                                            antibacterial; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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08-NOV-1997;
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Local Sim
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                                                                                                                                                                                    RESULT 64
ABP39236
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us-10-024-955-7.rag

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABH30511), expressed DNA sequences (ABL16176-ABH30511), expressed DNA ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
1256 IBIIVRQMLQKVRITDPGDTTLLFGEDVDKKEFYEENRRTEEDGGKPAQAVPVLLGITKA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806 DYGPESRGFVENSY----LAGLIPSEFYFHANGG-REGLIDTAVKTAETGYIQRRLIKA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 D-----IVSMEYDLAYKLGDLHPTT---HVISDIQDFVVALSLEISDEGNI-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHA--DKFERHVGIV-----DFKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GDANVKGEE---GIVKAHLLIGVHD
                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1887;
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                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster polypeptide SEQ ID NO 1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 84.5; DB
Pred. No. 36;
33; Mismatches
                                                                                   1316 SLGTESFISAASPODT----TRVLTDA 1338
                                                205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EW;
                                              178 IFGVLSDVLTAIFQDTVRKEMTKVLAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ELAMRNI-EARGLKOMKRO------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers
                                                                                                                                                                                                    ABB58245 standard; protein; 1887 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Sco.
22.7%; Prective 33; I
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                            26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
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                                                                                                                                                                                                                                                   ABB58245;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye plaseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, versicallymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases
         | ::: | | ::: | | ::: | K-----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTVIIMTSRNGAQ 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine, eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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                                                                                                                                                                                                                                                                                                                                                               Protein involved in intermediate metabolism of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 VAL-----SLEISDEGNITM---TSFEVROFANV---VNHIGG----
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                                                                                                        173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 84.5; DB
Pred. No. 23;
34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 739-741; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of Chlamydia trachomatis.
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                                                                                                                                                                                                                                     standard; protein; 1396
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97FR-00016034.
98US-0107077P.
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es 49; Conserv
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17-DEC-1997;
04-NOV-1998;
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                                       615
                                                                                                                                                                                                                                     AAY36871
                                                                                                                                                                                                                                                                              AAY36871;
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                                                                                                                                                                                         RESULT 65
                                                                                                                                                                                                                AAY36871

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AAY36871

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AAY368
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Gaps

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745 109 805 153

69

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DPIHYDKITEEINKAI-DDAIAAIEQSETIDPMKVPDHADKFERHVGI-VDFKGELAMRN

18

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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiee) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5883 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detectmine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be streptococcus that its prevented or treated may be meningitis. Nucleic stid encoding (I) may be used to recombinantly produce (I) and may be caid encoding (I) may be used to recombinantly produce (I) and may be chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                         Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antlinflammatory; infection; vaccine; meningitis; gene therapy.
   184
                              860 MESVAVAYDGTVRÁSVGÓLIQLRYGEDGLCGELVEFQNAPTVKLSNKSFEKRFKFDMSNE 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.9%; Score 84; DB 5; Length 306; Best Local Similarity 23.8%; Pred. No. 3.1; Matches 34; Conservative 25; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telford J, Masignani V, Margarit Y RosI,
Tettelin H;
                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 3268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 3480-3481; 4525pp; English.
                                                                                                                                                                                               ABP27046 standard; protein; 306 AA.
MISFEVROFANVVNHIGGLSIL-
                                                                                             920 RLMKKVFTDDVIKEMT 935
                                                                     185 -VLTAIFODTVRKEMT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001; 2001WO-GB004789
                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-352536/38.
N-PSDB; ABN67677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200234771-A2.
                                                                                                                                                                                                                                                                    02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAY-2002.
                                                                                                                                                                                                                                    ABP27046;
                                                                                                                                                           RESULT 67
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203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 MRNIBARGLKQWKRQGDANVKGEEGIVKAH----LLIGVHDDIVSME--YDLAYKLGDL- 125 : | : : | : : | !: : | : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                           204 LSKDKIKQEVKE----SYERLLKDSPQAG----VEVSYDSNYLLGFLINTLADSQTT
IEARGIKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLG-----DLHPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AVSADPIHYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                           Antibacterial; vaccine; gene therapy; infection; sepsie; diagnosis; enzymatic assay; antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.9%; Score 84; DB 6; Length 397;
.larity 24.1%; Pred. No. 4.4;
Conservative 35; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2726; 49pp; English.
                                                                                                             129 THVISDIODFVVALSLEISDEGN 151
                                                                                                                                         ROLLSDMSQATVGMPFSQFHEGH 275
                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus protein #1363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ
                                                                                                                                                                                                                          ABM72123 standard; protein; 397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001; 2001GB-00007661.
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-120786/11.
N-PSDB; ACF73683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200294868-A2
                                                                                                                                                                                                                                                                                          20-NOV-2003
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                                                                                                                                                                                                                                                           ABM72123;
                                             16
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Matches
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This invention describes novel human nucleic acid (CDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer; (in) directly for treating these forms of cancer (in) directly for treating these forms of cancer (in) appending expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY59941-Y60328 represent protein fragments encoded by the human endometrium tumour cDNA library derived EST fragments represented in AAZ41981-Z42121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid sequences expressed in uterine cancer tissues, and ved polypeptides, for treatment of uterine and endometrial cancer and
                                                               :: | | :: | | :: | | :: | | 190 XDPKYLIGRI----IARPY-VGEPGNFTRISNRHDYALKPFGKTVLDHLKDGGYDVI--A 242
130 VANKPASGTQIIDEWGEHQMKTGDLIVYTSADPVLQIAAHEDIIPLEELYDICEKVRELT 189
                                         126 HPTTHVISDIQDFVVALSLEISDEGNITMTS----FEVRQFA-NVVNHI--GGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahl
                                                                                                                                                                                                                                                                                                                                                                                                                                 Endometrium, human, tumour, cancer, anticancer, cytostatic, EST: treatment, uterine, gene therapy, expressed sequence tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 84; DB 2; Length 410; 22.1%; Pred. No. 4.6; ive 33; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                               encoded protein 56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived polypeptides, for treatment or identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hinzmann B,
                                                                                                                                                                                                                                                                       AAY59996 standard; protein; 410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 23; Page 297; 444pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98DE-01017948.
                                                                                                                                                                                                                                                                                                                                                                                               Human endometrium tumour EST
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Best Local Similarity 22.15
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                            179 FGVLSDV 185
                                                                                                                                                      | ::|:
243 IGKINDI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-591957/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 410 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE19817948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-OCT-1999.
                                                                                                                                                                                                                                                                                                              AAY59996;
                                                                                                                                                                                                                                RESULT 69
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The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-CCT-2001) which is available in flet witho.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                            401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 DQFGFINYEVGDSKKLFFHVKEVQD---GIBLQAGDE-----VEFSVIPKSSGGL
                                                   -----YKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVNHIGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleotide sequence useful in the identification or Lactococcus lactis and related species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                  Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 YDKITEBINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL---
LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Renault P, Ehrlich SD;
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Pred. No. 11;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 587; 2504pp; French.
                                                                                                                                                                                                            ABB53885 standard; protein; 775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Scor
19.8%; Pred
                                                                                                                                                                                                                                                                                                            Lactococcus lactis protein yfgQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2000; 2000FR-00004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2000; 2000FR-00004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 IEARGLKOMKROGD----
                                                                                                                                                                                                                                                                                                                                                              Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 19.89
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorokine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-043418/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 775 AA;
                                                                                                                                         A 402
                                                                                                             173 S 173
                                                                                                                                                                                                                                                                                                                                                                                            FR2807446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001.
                                                                                                                                                                                                                                                                 29-AUG-2003
16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bolotine A,
                                                                                                                                         402
                                                                                                                                                                                                                                        ABB53885;
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VSADPIHYDKITEEINKAIDDALAAIEQSETIDPMKVPDHAD-KFERHVGIV---DFKGE 70

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The invention relates to the gene cluster encoding the polypeptides responsible for the biosynthesis of the polyene antibiotic amphotericin responsible for the biosynthesis of the polyene antibiotic amphotericin useful for preparing amphotericin derivatives or analogue antibiotic amphotericins with altered properties and in the biosynthesis of polykeides other than amphotericin ampholIII, ampholII or amphoII amphotericin derivatives glycosylated with alternative sugars; amphoIII or amphoII 
                                                                                         PDQKRRLVQALKRKDHTVAMTGBGVNDILAMKSADCSIAMASGSDAATQVAQVVLLDSDF 574
                                                                                                                                                              GNITMISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTK-----V 201
                                                                                                                                                                                             GHMTQVVTEGRRVVNNVQRSAILFLVKNLFSIILAIISAIFVFTYPLQASQLSLISLFTI 634
  FAEQGVNIKVISGDNPQTVSAVAKRAGITGAERFIDANLLKTKEDLDQAVESYTVFGRVT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel cytochrome P450 enzyme and nucleotides encoding the enzyme, useful for preparing amphotericin derivative or analog antibiotic agent with altered properties, in biosynthesis of polyketide other than
                                                      -----IGVHDDIVSMEYD----LAYKLGDLHPTTHVISDIQDFVVALSLEISDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polyene; antibiotic; amphotericin; amph; polyketide synthase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.9%; Score 84; DB 6; Length 9510; Best Local Similarity 24.5%; Pred. No. 4e+02; Matches 53; Conservative 39; Mismatches 80; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces nodosus amphI gene encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 120-162; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE36119 standard; protein; 9510 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2001; 2001IE-00000527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAY-2002; 2002WO-IE000071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYDU-) UNIV COLLEGE DUBLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                        LAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                         635 GIPGFLLSLEEN 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces nodosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-201271/19.
N-PSDB; AAD54645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200297082-A2
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The present invention provides a number of nucleotide and protein are quences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                 :| : || | | : : |
582 RFPVFAAALDAALDAFTPHLDVPLRKVLWGEDADRLDRTEYAQPALFAVEVALYRLLESF 641
                                                              45 TIDPMKVPDHA--DKFERHVGIVDFKGELAMRNIEARG-LKQMKRQGDANVKGEEGIVKA 101
 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polymucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                             642 EVKPDHLAGHSVGEIAAAHVAGV-FSLDDAATLVAARGRLMQALPEGGAMVAVQASEDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ochiai K, Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.
                                                                                                                            102 HLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNIT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; SEQ ID NO 3526; 246pp + Sequence Listing; English
                                                                                                                                                                                             185
                                                                                                                                                                                                              KFLLIAAVAFVAVSADPIHYD----KIT--EEINK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                                                                                                                                                                          protein fragment SEQ ID NO: 3526.
                                                                                                                                                                                             154 ----MISFEVROFANVVNHIGGLSILDPIFGVLSDV
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                                                                                                                                                                                                                                                                                                          AAG89772 standard; protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-00377484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2000; 2000EP-00127688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mizoguchi B
Senoh A,
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N-PSDB; AAH64991.
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                                                                                                                                                                                                                                                                                                                                                                                                           glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
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Tateishi N
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Length 412;

DB 4;

Score 83.5;

7.88;

Query Match

10;

Gaps

44;

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183

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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to muclaic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the invention of compounds that modulate the invention; methods for the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC32628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                      54 HADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                       Human, diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; uno steoporosis; autoimmune disease; cancer; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                         ---- OWEEGSARPVAALGVSDN-VS
                   17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wehrman T;
                                                                                                                               114 MEYDLAYKLGDLHPTTHVISDI-----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                              184 YTYDINRPIGD-RVTSVTIDDTPLDPERDYVVAASLYL-QSGNEGMTA 229
                 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J,
Wang Z,
                                                                                                                                                                                                                                                                                                                                                                     Human novel polypeptide sequence, SEQ ID NO:1069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Zhao QA,
Asundi V,
                                                                            31.5%; Pred. No. 5.3; tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; SEQ ID NO 1069; 1185pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TY, Zhang J, Ren F, Xue AJ, P, Ghosh M, Wang D, Ma Y, Ay-Vicente D, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; chromosome 15q21.3.
                                                                                                                                                                                                                                                            ADC30987 standard; protein; 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2002; 2002WO-US030474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-SEP-2001; 2001US-0324631P.
                     Conservative
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 Best Local Similarity
Matches 34; Conserv
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                     34;
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                                                                                                                                                                                                                                          ADC30987
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useful in diagnostics, drug screening, forenaics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are disease and other neurodegenerative diseases, anaemia, platelet disease and other neurodegenerative diseases, anaemia, platelet cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence of the invention. Note: The sequence was obtained in electronic format directly from WIPO at the published_pot_sequence.
                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                    160 HLGKTIEKLQKEMADIVEASRTSTLELQNQLDEYKERNRRE--LAEMQRQLKEKTLEAEK 217
                                                                                                                                                                                                                                                                                                                                                                                                                            80 -GLKQMKRQGDANVKGE------EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                               21 HYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                 Indels 17; Gaps
                                                                                                                                                                                                                                                                                                      Length 517;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #36108.
                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                     DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                     7.8%; Score 83.5; DE 21.7%; Pred. No. 7.3; ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 THVISDIQDFVVALSLEISDEGN 151
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00948993.
2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                    Local Similarity 21.7
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-029926/02
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                                                                                                                                                                                                                                                                       Sequence 517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yersinia pestis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAR-2002;
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                                                                                                                                                                                                                                                                                                      Query Match
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Wall D,
                                                                                                                                                                                                                                                                                                                                    Matches
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                                                    The invention relates to an isolated nucleic acid compitising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation or that has an activity against a biological pathway required for proliferation or the the test compound that inhibits spoilferation of an organism the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for underexpressed, it underexpressed, it is a compound that inhibits the proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the contine of an organism. The antisense uncleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. prenumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequence of the target proverded proverded proverded proverded 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 PETGSIELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATL---- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VAVSADPIHYDKITEEINKAIDDA-IAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; structural and cytoskeleton-associated protein; SCAP; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; myelofibrosis; psoriasis; cancer; pueumonia; chronic bronchitis; yellow fever; influenza; meaales; mumps; HIV; human T lymphotropic virus; rabies; gastroenteritis; encephalitis; rubella; epilepsy;
                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 RQFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human structural and cytoskeleton-associated protein (SCAP) #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.8%; Score 83.5; DB 6; Length 548; 18.1%; Pred. No. 7.9; tive 45; Mismatches 80; Indels 69
                Claim 25; SEQ ID NO 78505; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE15622 standard; protein; 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 18.19
les 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE15622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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The invention comprises the amino acid and coding sequences of human structural and cytoskeleton-associated proteins (SCAP). The SCAP DNA and protein sequences of the invention are useful for the diagnosis and treatment of: arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, myelofibrosis, psoriasis, grimary cancer, pneumonia, chronic bronchitis, yellow fever, influenca, measles, mumps, HIV, human T lymphotropic virus, rabies, gastroenteritis, encephalitis, rubella, epilepsy, ischaemic cerebrovascular disease, stroke, cerebral neoplasm, Alzheimer's disease, Pick's disease, Pick's disease, Pick's disease, pick's disease, solerosis, meningtis, brain abscess, prion disease, Creutzfeldt-Jakob disease, insomnia, neurofibromatosis, cerebral palsy, myasthenia gravis, anxiety. The present amino acid sequence represents a human SCAP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 -GLKQMKRQGDANVKGE-----EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT 128
ischaemic cerebrovascular disease; stroke; cerebral neoplasm;
Alzheimer's disease; Pick's disease; Huntington's disease; dementia;
Parktinson's disease; amyotrophic lateral sclerosis; atrophy;
hereditary ataxia; multiple sclerosis; meningitis; brain abscess;
prion disease; Creutzfeldt-Jakob disease; insomnia; neurofibromatosis;
cerebral palsy; myasthenia gravis; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 HYDXITEBINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YI, Thangavelu K;
Hafalia AJA, Swarnakar A;
Lu DAM, Arvizu CS, Kable AE
son AA, Khare R, Elliott VS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polypeptides useful for treating e.g. cell disorders, viral infections and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yue H, Griffin JA, Richardson TW, Tang YT, Foreythe IJ, Becha SD, Chawla NK, Hafalia Marquis JP, Gorvad AE, Baudon NK, Lu DAM, Lee SY, Ramkumar J, Jiang X, Jackson AA, Bulloch SA, Xu Y, Lee S, Lehr-Mason PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.8%; Score 83.5; D
21.7%; Pred. No. 13;
ive 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 THVISDIQDFVVALSLEISDEGN 151
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2002US-0381599P.
2002US-0387270P.
2002US-0397125P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramkumar J, Jiang
A, Xu Y, Lee S,
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Best Local Similarity 21.7
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-671468/63.
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                                                                                                                                                                                                                                                                                                WO2003062391-A2
                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2002;
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164 TQMLFAHHGLTLRDKK--APSVFFVKKLKNTLNHVYGYAVL----SISSKQLANLFQSVV 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 190-192; 193pp; English.
                                                                                                                                                                                                             AAU71861 standard; protein; 845 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-APR-2000; 2000US-00551974.
05-MAY-2000; 2000US-00565501.
14-AUG-2000; 2000US-00639206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001; 2001WO-US011254
                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campos-Neto A,
                                                 RKEMTKV 201
                                                                                           NPEISKI 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probst P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-061971/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAS96071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 845 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200179276-A2.
                                                                                                                                                                                                                                                                                                         26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2001.
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Coler RM,
                                                 195
                                                                                                                                                                                                                                                          AAU71861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid derived from Enterococcus faccium encoding an Enterococcus faccium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included are a recombinant vector comprising the nucleic acid operably linked to transcription requlatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids is useful for diagnosing pathological conditions. The nucleic acids is useful for diagnosing pathological conditions infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection, and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans of and vaccines conteaining the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents con it the back of the nucleic acid is useful to recombinant the present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 QGDANVK------GEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISD 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated nucleic acid derived from Enterococcus faecium encoding erococcus faecium polypeptide useful for detection, prevention and ntment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Gaps
                                                                                                                                                                                                                               Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 83; DB 7; Length 583; 18.7%; Pred. No. 9.8; tive 36; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 5678; 243pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating Enterococcus faecium infections. one if the disclosed E. faecium proteins.
                                                                                                                                                                                         ID 5678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
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                                               ADC96051 standard, protein; 583
                                                                                                                                                                                         E. faecium protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0051571P.
98US-0085598P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00107532.
                                                                                                                                          (first entry)
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Best Local Similarity 18.73
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bush
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                                                                                                                                                                                                                                                                                                         Enterococcus faecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADC92397.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus
treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-1997;
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                                                                                                                                          01-JAN-2004
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                                                                                           ADC96051;
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                      ADC96051

ADC9 ADC ADC9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 845;
17:
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Leishmania antigen 4G2-83 extended protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Mismatches
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10;

Gaps

34;

70;

34; Mismatches

Conservative

88 52 144

DANV----KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL

204

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53 DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
                                                  2 VNFTVDQVRELMDYPDQIRNMSVIAHVD------HGKSTLSDSLVGAAGIIXMEEAG
                                                                                                                                             145 EISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                              29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
   42;
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   Matches
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ADB78873
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treating
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel polypeptide containing an immunogenic portion of a Leishmania antigen or its variant which has antiparasitic and immunostimulant activity. The compositions and methods of the present invention are useful for preventing, treating and detecting invention are useful for preventing, treating and detecting leishmaniasis, and stimulating immune responses in patients against leishmaniasis. The polypeptides and the polymucleotides encoding them can be used for gene therapy, in vaccines or as interleukin-12 agonists. The compositions and methods of the present invention, as compared to prior art, are more improved therapeutic modalities in the diagnosis, prevention and treatment of leishmaniasis
                - IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL-----RQALTERIRP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon DC, Skeiky YAW, Bhatia A;
 EISDEGNITMISFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                                                                                                                                                                                                                Antigen; immunogenic; antiparasitic; immunostimulant; leishmaniasis; gene therapy; vaccine; interleukin-12 agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide containing at least an immunogenic portion of
Leishmania antigens or their variants, useful for preventing,
and detecting leishmaniasis, and stimulating immune responses
                                                                                                                                                                                     major 4G2-83 extended antigen SEQ ID 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 108-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Webb JR,
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Probst P, Brannon M;
                                                                                                 AAB71315 standard; protein; 845
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12-FEB-1997; 97US-00798841.
12-FEB-1998; 97US-00022765.
30-GCT-1998; 98US-00183861.
14-ARR-2000; 2000US-00551974.
65-MAX-2000; 2000US-0055551.
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                                                                                                                                                           entry)
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CAMPOS-NETO A.
WEBB J R.
DILLON D C.
SKEIKY Y A W.
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PROBST P.
BRANNON M.
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                                                                                                                                                                                                                                                           Leishmania major.
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Coler RN,
 145
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(SKEI/)
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(WEBB/)
                                                                     RESULT
AAB7131
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Length 845;

Score 83; DB 5; Pred. No. 17;

7.8%;

Query Match Best Local Similarity

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The invention relates to an isolated polypeptide comprising an immunogenic portion of a Leishmania antigen or its. Also included are antigenic epitopes, fusion proteins comprising an isolated polypeptide fusion protein comprising at least two contiguous antigenic epitopes, polynucleotides encoding the antigens or fusion proteins, a recombinant expression vector comprising the polynucleotide, a host cell transformed with the vector and a composition (pharmaceutical or immunogenic) comprising the antigen or fusion protein and a physiologically acceptable carrier. The compositions are useful for inducing protective immunity
             151
                                                                                                                                                                                                           Antigen, protozoacide, antibacterial, virucide, cytostatic, immunostimulant, leishmaniasis, Leishmania infection, immune response, interleukin-2 stimulation, cancer; bacterial infection, viral infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated polypeptide useful for preventing or treating leishmaniasis, comprises an immunogenic portion of a Leishmania antigen
101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP
                                                                                                                                                                               Leishmania T cell antigen 4G2-83 extended protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 110-112; 183pp; English.
                                                                                       ADB78873 standard; protein; 845 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                             95US-00533669.
97US-00798841.
97US-00920609.
98US-00022765.
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05-MAY-2000; 2000US-00565501.
14-AUG-2000; 2000US-00639206.
04-JUN-2001; 2001US-00874923.
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                                                                                                                                                    (first entry)
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CAMPOS-NETO A.
WEBB J R.
DILLON D C.
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                                                                                                                                                                                                                                                            protozoan infection
                                                                                                                                                                                                                                                                                         Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leishmaniasis,
or its variant
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12-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                    14-NOV-2002
                                                                                                                     ADB78873;
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(WEBB/)
(DILL/)
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against leishmaniasis in a patient. The fusion protein is useful for the detecting Leishmania infection in a patient by contacting dermal calls of the patient with the composition and detecting an immune response on the patient's skin, where the immune response is induration. The compositions are useful for stimulating a cellular and/or humoral immune response in a patient, or for treating a cellular and/or humoral immune response in a interleukin (IL)-2 stimulation, where the disease responsive to interleukin (IL) as bacterial, wirsh or protozoan infection. The antigen is useful for preventing or treating leishmaniasis. The present sequence represents a Leishmania antigen (or fragment).
                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : :| | : | | : | | DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
                                                                                                                                                                                                                                                                                                                                                    34; Gaps
                                                                                                                                                                                                                                                                                                   Length 845;
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                                                                                                                                                                                                                                                                                                 DB 7;
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                                                                                                                                                                                                                                                                                                                                                 42; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                            Seguence 845 AA;
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Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
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                                                                                                                                                             Renault P,
           ABB53805 standard; protein; 1060 AA
                                                       Lactococcus lactis protein dnaE.
                                                                                                                       11-APR-2000; 2000FR-00004630,
                                                                                                                                   11-APR-2000; 2000FR-00004630.
                                                                                 Lactococcus lactis; IL1403
                                            (first entry)
                                                                                                                                                             Sorokine A,
                                     (revised)
                                                                                                                                                             Bolotine A,
                                                                                              FR2807446-A1
                                     29-AUG-2003
                                                                                                          12-OCT-2001.
                                           16-MAY-2002
                        ABB53805;
     RESULT
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New nucleotide sequence useful in the identification or Lactococcus lactis and related species. WPI; 2002-043418/06.

Ehrlich SD;

The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB5300-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese. Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in Claim 6; SEQ ID NO 507; 2504pp; French.

.. 8 91 NVKGE----EGIVKAHLLIGVHDDIVSMEYDLAYK-----LGDLHPTTHVISDIQDF-- 138 59 QPIISIELNFEWRGLPIAFSFIAKDTEGYKNLLRISTLHNYGRRQFSDIQNHLSGIALII 118 The GroEL heat shock protein (AAW16678) of Lawsonia intracellularis can be used in vaccines to protect birds and animals against intestinal diseases, esp. to protect pigs against porcine proliferative enteropathy. It is the expression product of a DNA molecule (AAT6201) obtd. by screening an L. intracellularis library with rabbit anti-L. intracellularis sera. GroEL, GroES (AAW16679) and other L. intracellularis polypeptides (AAW1660-85) can be administered as recombinant polypeptides or expressed as recombinant vaccines utilising bolypeptides or viral vectors. Antibodies raised against the polypeptides may be useful in immunotherapy, diagnosis of infection and detection -----NI----TMTSFEVROFANVVNHIGGLSILD 176 28 Vaccine for treating or preventing Lawsonia intracellularis infection -especially in pigs, containing non-pathogenic form of bacterium or its Intestinal disease; porcine proliferative enteropathy; vaccine; GroEL; immunotherapy; antibody; diagnosis; heat shock protein. 6 NIKTEYSFLDSVVKV-----DDYLETAHRLGYQTVGICDVGNLHAAFRFVRKAQKFNL electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field) Gaps 52; Length 1060; Indels 38; 5; P-IFGVLSDVLTAIFQDTVRKÉMTKVLAPAF 206 119 PETYGSLSEL-----TELSSVADEAF 139 ; Score 83; DB ; Pred. No. 23; 29; Mismatches Claim 10; Page 38-42; 94pp; English. AAW16678 standard; protein; 548 AA 96WO-AU000767. 7.8%; 95AU-00006910. 95AU-00006911. 139 ---WALSLEISDEG----(DARA-) DARATECH PTY LTD. (PIGR-) PIG RES & DEV CORP. (first entry) Query Match 7.8 Best Local Similarity 21.2 Matches 32; Conservative Lawsonia intracellularis WPI; 1997-310605/28. N-PSDB; AAT69201. Sequence 1060 AA; 29-NOV-1996; 30-NOV-1995; WO9720050-A1 30-NOV-1995; 20-AUG-1997 05-JUN-1997. Panaccio M, components 177 AAW16678; RESULT 81 AAW16678 88000 g 8 ઠ

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Human; drug metabolising enzyme; anti-HIV; antiallergic; antidiarmatory; antianeamic; thrombolytic; antilipsemic; antidiarmatory; antianeamic; thrombolytic; antilipsemic; antidiared; cytostatic; hepatotropic; antiathmatic; immunosupressive; antidiabetic; exptostatic; hepatotropic; virucide; dermatological; antidiabetic; antigout; neuroprotective; thromimetic; osteopathic; antiarthritic; antipooriatic; uropathic; ophthalmological; antirheumatic; haemostatic; gene therapy; cell proliferative disorder; cancer; metabolic disorder; andocrine disorder; andisorder; antipooriatic disorder; autolimmune disorder; ilver disorder; autolimmune disorder; ilver disorder; bME-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human drug metabolising enzyme, DME-2, SEQ ID 2.
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Best Local Similarity
Matches 39; Conserv
 N-PSDB; ABX34508
                                                                                                                                                                                                                                                                                                                                                                  Sequence 953 AA;
                                                                  or hepatitis.
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                                                                                             ELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAY----- 120
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                                                                                                                                                                                       -----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVR 160
                                                                                                                                                                                                       209 EKMYCELDNPYILCNEKKITSMKDMLPILEQVAKYNRPLLIIAEDVEGEALATL----- 262
                                                                                                                                                                                                                                                                     ----VVNKLRGALQVVAVKAPGFGERRKAMLEDIAILTGGEAIFEDRGIKLENVSLSSLG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytosfatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adehocarcinoma; leukaemia; lymphoma; melanoma; mysloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; AIDS;
                                                                               10 VAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKG 69
                                                                                                                                                                                                                                           161 QFANVVNHIGG----LSILDPIFG-----VLSD--VLT---AIFQD-----
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, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
H, David MH, Lewis SA, Chen AJ, Penzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urasaka ME;
                                                   87;
                           DB 2; Length 548;
                                                   83; Indels
                         Score 82.5; D; Pred. No. 10; 43; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MDDT polypeptide SEQ ID 465.
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29-WAY-2001, 2001US-0280068P.
16-WAY-2001, 2001US-0291280P.
17-WAY-2001, 2001US-0291829P.
17-WAY-2001, 2001US-0291849P.
19-UNN-2001, 2001US-029948P.
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                                                   49; Conservative
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Dufour GE, Hillman.
Daugherty SC, Dam TC, I
Peralta CH, David MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 psoriasis; hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-058431/05
                        Query Match
Best Local Similarity
Matches 49; Conserv
Sequence 548 AA;
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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, catteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic, antianaemic, antipsoriatic and heparotropic activity. The polymucleotides cand the polypeptides of the invention can be used for gene therapy, of protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polymucleotides are particularly useful for diagnosing, treating or preventing call proliferative disorders (e.g. cancers including adenocarcinoma, lumphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's clusaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's syndromes, inflammation, osteoporosis, thrombocycopaenia, psoriasis or hepatitis. ABUI1450-ABUI1845 represent the MDDT polymucleotides encoded by ABUI1450-ABUI1845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            764 DKDRKDLBGRLKAR----EDLLLPIYHQVAVQFADFHDTPGRMLEKGVISDILEWKTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-----THVISDIQDFVVAL
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                                                                                                                                                                                                                                Claim 27; SEQ ID NO 465; 339pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELYWRLRRLLLEDO----VKOBILQASGELSHVHIQSML 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 S-----LEISDEGNITMTSFEVROFANVVNHIGGLSIL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 82.5; D 24.2%; Pred. No. 22; iive 32; Mismatches
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us-10-024-955-7.rag

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acides encoding the polypeptides and calls genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used to an unitional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                      Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration; immune suppression, immune stimulation, anti-inflammatory, leukaemia.
Novel human secreted protein #3339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 678; 765pp; English.
                                                                                                                                                                                                                                                                         16-APR-2001; 2001WO-US008656.
                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000US-00552929.
26-JAN-2001; 2001US-00770160.
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                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                 WO200179449-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                             25-OCT-2001
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DME-1 to DME-13 (ABP59210-ABB5922) and their coding sequences (ABZ81311). The sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME, particularly cell proliferative disorders (a arteriosalerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria, atherosalerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria, colopmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), endocrine (e.g. orteoporosis, thrombocytopenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), endocrine (e.g. orteoporosis, thrombosis, diabetes), ed disorders (e.g. gratrointestinal disorders (e.g. spatrointestinal disorders (e.g. spatroenteritis, diarrhosa), liver disorders (e.g. hepatitis, Reye's syndrome), or autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, oftense bronditis, parocreatitis, Reye's syndrome, multiple sclerosis, stormore syndrome, uveitis). They are also useful in the assessing the effects of exogenous compounds on the expression of mucleic acid and for more also sequences of DME. The polymucleotides encoding DME are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to novel human drug metabolising enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2210 TINPLCIEMYADK-ESRGGVLEPEGTVEIKFRKKDLIKSMRRIDPAYKKIMEQLGEPDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----THVISDIQDFVVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      New drug metabolizing enzymes (DME) useful for diagnosing, treating preventing diseases or conditions associated with aberrant DME expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma, hepatitis or osteoporosis.
                                                                                                                                                                                                    Griffin JA, Ramkumar J, Emerling BM, Richardson TW, Li JX; warren BA, Honchell CD, Baughn WR, Tang YT, Lee EA, Elliott VS Yue H, Lee S, Swarnakar A, Forsythe IJ, Sanjanwala MM, Yao MG; Zebarjadian Y, Gorvad AE, Becha SD, Burford N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 2458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences of DME. The polynucleotides encod for creating transgenic animals to model human disease
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24.2%; Pred. No. 85;
tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 149-155; 181pp; English.
                                         06-JUL-2001; 2001US-0303745P.
13-JUL-2001; 2001US-0305402P.
13-JUL-2001; 2001US-0305158P.
14-SEP-2001; 2001US-0322127P.
05-JUL-2002; 2002WO-US021105
                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 24.2
Matches 39; Conservative
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Drmanac RT;

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----THVISDIQDFVVAL
                                                                                  ----AMRNIEARGLKOMKROG----
                          DB 4; Length 2486;
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                                                                                                                                        DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT
                                                     49;
                                      Pred. No. 87;
                                                                                  45 TIDPMKVPDHADKFERHVGIVDFKGEL-----
                       7.7%; Score 82.5;
24.2%; Pred. No. 87
tive 32; Mismatche
                                                                                                                                                                                                                                                                                             ABB84649 standard; protein; 2487 AA.
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                                                    39; Conservative
                                        Local Similarity
Sequence 2486 AA;
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2269 DXDRKDLEGRLKAR----EDLLLPIYHOVAVOPADFHDTPGRMLEKGVISDILEWKTAR 2323

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2324 TFLYWRLRRLLLEDQ-----VKQEILQASGELSHVHIQSML 2359

AAU32848 standard; protein; 2486 AA

18-DEC-2001

143 S-----LEISDEGNITMTSFEVROFANVVNHIGGLSIL 175

mapping naturally occurring genomic sequences. ABB84649-ABB84673 represent secreted proteins encoded by the cDNA's shown in ABS57545-ABS57569, described in the disclosure of the invention

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Human SECP-1 protein from clone 7757335CD1 SEQ ID 1.
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Secreted protein; SECP; human, antiarteriosclerotic; antiatherosclerotic; hepatotropic; oytostatic; anti-HIV; antiallergic; antiaschmatic; cancer; antianemic; antidabetic; antiflammatory; neuroprotective; antiulcer; antitheumatic; antiathritic; cardiant; hypotensive; gonadal dysgenesis; vasotropic; anticonvulsant; nootropic; immunosuppressive; pericarditis; antiparkinsonian; ophthalmological; cell proliferative disorder; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; angina pectoris; autoimmune disorder; AIDS; Crohn's disease; multiple sclerosis; epilepsy; ulcerative colitis; cardiovascular disorder; myocardial infarction; Raymaud's disease; myocarditis; neurological disorder; cataract; Huntington's disease; Alzheimer's disease; Crettzfeldt-Jakob disease; developmental disorder; Duchenne muscular dystrophy; antipsoriatic; Becker muscular dystrophy; Cushing's syndrome.

Homo sapiens.

WO200279441-A2

10-OCT-2002

29-MAR-2002; 2002WO-US009820

30-MAR-2001; 2001US-0280527P. 06-APR-2001; 2001US-0282112P. 09-APR-2001; 2001US-0282702P. 13-APR-2001; 2001US-02838SSP. 19-GCT-2001; 2001US-0343718P. 17-DEC-2001; 2001US-0339236P. 13-FEB-2002; 2002US-0357002P.

(INCY-) INCYTE GENOMICS INC.

Jan BM, Elliott VS, Forsythe IJ;
He A, Honchell CD, Ison CH;
SEON FW, Sanjanwala MM;
Thangavelu K, Tran UK, Walia NK; Baughn MR, Burford N, Ding L, Duggan BM, I Gandhi AR, Gietzen KJ, Griffin JA, He A, I Lal PG, Lee EA, Lee S, Lu DAM, Mason PM, Barrankar A, Ramkumar J, Tang YT, Thangavei Warren BA, Yao MG, Xu Y, Yue H;

2003-058429/05. WPI; 2003-058429/ N-PSDB; ABS57545 Novel human secreted protein useful for treating, preventing or diagnosing cancer, hepatitis, psoriasis, asthma, diabetes mellitus, anemia, epilepsy, cataract, Alzheimer's disease.

Claim 56; Page 143-149; 188pp; English.

This invention describes novel secreted proteins (SDCP) which have antiarteriosclerotic, antiatherosclerotic, hepatotropic, cytostatic, antiarteriosclerotic, antiathmatic, antialabetic, antidiabetic, antidiabetic, antiathmatory, neuroprotective, antialcer, antipseriatic, vasotropic, antiarthritic, cardiant, hypotensive, anticonvulsant, nootropic, immunosuppressive, antiparkinsonian and ophthalmological.

Continity The polymucleotides and polypeptides of the invention can be cativity. The polymucleotides and polypeptides of the invention can be used for diagnosing, treating or preventing cell proliferative disorder.

Continity antialist, anticonsist, atherosclerosis, directions, disorder.

Continumune/inflammatory disorders e.g. acquired immunodeficiency syndrome attoinmunne/inflammatory disorders e.g. acquired immunodeficiency syndrome conditives allerosis, ulcerative colitis, psoriasis, rheumatorial anticonders active colitis, psoriasis, rheumatorial anticonders e.g. myocardial infarction, angina pectoris, hypertension, Raymaud's disease, myocardial infarction, angina pectoris, contrological disorders e.g. puchenne and Becker muscular dystrophy, disease, Alzheimer's disease, Creutzfeldt-Jakob disease, etc; and developmental disorders e.g. Duchenne and Becker muscular dystrophy, caterator, gonadal dysgenseis, contrological disorders e.g. cateratory and also be used for drug sorreening, proteome analysis, microarrays creating knock-in humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in commal, carrier or affected individuals, and as hybridization probes for normal,

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                                                                                                                                                                                                                                                                                                                                                                                         NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer; hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                             89 DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT----THVISDIQDFVVAL
                                                                                                                                                                                                                                                         45 TIDPMKVPDHADKFERHVGIVDFKGEL------AMRNIEARGLKOMKROG----
                                                                                                                                                                                                       Gaps
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                                                                                                                                                7.7%; Score 82.5; DB 6; Length 2487; 24.2%; Pred. No. 87; ive 32; Mismatches 49; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 S-----LEISDEGNITMTSFEVRQFANVVNHIGGLSIL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU65149 standard; protein; 2498 AA
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2001US-0275235P.
2001US-0275578F.
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2001US-0275601P.
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2001US-0280900P
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                                                                                                                                                                                 1 Similarity 24.23
39; Conservative
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                                                                                                      Sequence 2487 AA;
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12-MAR-2001;
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13-MAR-2001;
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08-MAR-2001;
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02-APR-2001;
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                                                                                                                                                     Query Match
Best Local S:
Matches 39,
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2001US-0283675P.
2001US-028966P.
2001US-0288528P.
2001US-0291190P.
2001US-0291485P.
2001US-0294889P.
2001US-0294889P.
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200105-0293303P
200105-0349310P
200105-0349310P
200105-0312903P
200105-0318462P
200105-0318770P
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200105-0318770P
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2001US-0332172P.
2001US-0332271P.
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2001US-0333272P.
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2001US-0337426P.
                                                                                                                                                      2001US-0332272P
                                                                                                                                                                                                     2002US-00092900
                                                                                                                                                                                                                                                        Rieger DK;
                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                    2002-723332/78.
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                                                                                                                                                                                                                                                                          N-PSDB; ABX97116.
                                                                                                                              18-OCT-2001;
31-OCT-2001;
14-NOV-2001;
14-NOV-2001;
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14-NOV-2001
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                                                                                                                                                                                                                                                         Lepley DM,
                                        16-MAY-200
                                                          31-MAY-200
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Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                  NOVX polypeptides and polynucleotides, useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g., cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma.
           a CEA, Li L;
Kekuda R;
Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CBA, Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V, Ebernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 313-314; 1103pp; English.
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This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity esq. cancer, hypotension, atherosclerosis, cardiamyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABUGEO41-ABUGEO48 represent the NOVX polypeptides encoded by

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Sequence 2498 AA;
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7;
                                                                                                88
                                                                                                ---AMRNIEARGLKOMKROG----
                                               49; Indels 41; Gaps
Query Match 7.7%; Score 82.5; DB 5; Length 2498; Best Local Similarity 24.2%; Pred. No. 87; Matches 39; Conservative 32; Mismatches 49; Indels 41;
                                                                                                TIDPMKVPDHADKFERHVGIVDFKGEL-
                                                                                                45
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Gaps

30;

39; Indels

27; Mismatches

24.48;

Best Local Similarity 24.49 Matches 31; Conservative

Query Match

7.7%; Score 82; DB 4; Length 277;

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AAH52104 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the collypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymorleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polymorleotide sequences given in the cepture of the present experience of the present invention of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given the present of th
                                                                                         2250 TINPLCIEMYADK-ESRGGVLEPEGTVEIKFRKKDLIKSMRIDPAYKKLMEQLGEPDLS 2308
                                                     ----THVISDIQDFVVAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S. epidermidis open reading frame protein sequence SEQ ID NO:1988.
                                                                                                                                                                                                 : | : | : | | : | 2364 TFLYWRLRRLLLEDQ-----VKQEILQASGELSHVHIQSML 2399
                                                                                                                                                                   143 S-----LEISDEGNITMTSFEVRQFANVVNHIGGLSIL 175
                                                     DANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-
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                                                                                                                                                                                                                                                                                                                                                               AAG82447 standard; protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-2000; 2000WO-US030782.
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196 KEMTKVLAPAFKRE 209
                                                                  290 GDQLHILLTKWGKE 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 DANVKGEEGIVKAHILIGVHDDIVSME-----YDLAYKLGDLHPT-THVISDI 135
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MXRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL 142
                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused S. aureus, e.g. sepsis.
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                                                                                                                       173 AQQY--HAHVITTDFNL----NKVCHVQGITALN-----VNDLSBAIKPNVHQGDQLSIL
                                                                                              143 SLEISDEGNITMISFEVROFANVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 3434; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus protein #1717.
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                                                                                                                                                                                                                                                                                                                                                      ABM72477 standard; protein; 357 AA.
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                                                                                                                                                                                         203 APAFKRE 209
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N-PSDB; ACF74037.
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
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                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 MKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SLEISDEGNITWISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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                                                                                                                                                                                                              Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4057.
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7.7%; Score 82; DB 5; Length 362;
Best Local Similarity 24.4%; Pred. No. 6.4;
Matches 31; Conservative 27; Mismatches 39; Indels
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ABP39212 standard; protein; 362 AA.
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97US-0064964P.
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                                                                                                                                                                                                                                                                                                                                         antibacterial; gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis.
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us-10-024-955-7.rag

(revised)
(first entry)

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Chlamydia, lpdA; infection, diagnostic, medicament; gene therapy; antibacterial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY34584-V35879 represent the proteins encoded by all the open reading frames in the complete ganome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae. (Updated on 17-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                          Respiratory disease, pneumonia, bronchitis, heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum, pharyngitis, vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
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                                                                                                                                                                                                                                                                   Chlamydia pneumoniae transmembrane protein sequence.
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                                  AAY35476 standard; protein; 397
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AAB62188
ID AAB62188 standard, protein, 461
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13-SEP-1999
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AAY35476

AAY35476

AAY35476

AAY3

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99US-0154325P

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11;
                                                                                                                                                                                          Novel Chlamydia pneumoniae lpdA protein and polynucleotides encoding them useful as component of vaccines for treating Chlamydia infections, and for detecting Chlamydia infection in the body fluid of a mammal.
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                                                                                                                                                                                                                                                                                                                                                           This represents the Chlamydia pneumoniae 1pdA protein. The 1pdA protein can be expressed by standard recombinant methodology. The 1pdA protein, polyuucleotide and antibodies specific to the protein and vaccines comprising the 1pdA protein are useful for preventing or treating chlamydia (C. trachomatis, C. psittaci, C. pneumonia or C. pecorum) infection. Vaccine vectors, and the 1pdA protein are useful in the preparation of medicaments for preventing and/or treating Chlamydia infection. Primers and probes derived from the 1pdA gene are also useful for detecting and/or identifying Chlamydia in the biological material. (Updated on 11-SEP-2003 to standardise OS field)
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                                                        Wang J,
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(AVET ) AVENTIS PASTEUR LTD.
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Best Local Similarity 20.43.
The 46; Conservative
                                                        Comen RP,
                                                                                                             2001-257992/26.
                                                                                                                                           N-PSDB; AAF57425
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ABU27059;

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The present invention describes compositions comprising a Chlamydia Capi protein and methods for the diagnosis and therapy of Chlamydia infection. Chlamydia DNA and protein sequences from the present invention can have antibacterial and immunostimulant activities, and can be used in vaccines. Compounds from the present invention can be used for eliciting an immuno response, specifically stimulating a Chlamydia-specific. T-cell response or inhibiting the development of a Chlamydia infection in an presence of Chlamydia in patient; to stimulate and/or expand T cells specific for a Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia in a patient; to stimulate and/or expand T cells specific for a Chlamydia and ABB94096 to ABB94374 represent sequences used in the exemplification of the present invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                       Chlamydial infection, Chlamydia, vaccine, detection, diagnosis, antigen, antibacterial; immunostimulant, immune response, Chlamydia-specific T-cell response.
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                                                                      Chlamydia pneumoniae protein sequence SEQ ID NO:399.
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23-APR-2001; 2001US-00841132.
               (revised)
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                                                                                                                                                                              Chlamydophila pneumoniae.
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               29-AUG-2003
05-JUN-2002
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275
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                                                                                                                                                                                                                                                                                                                                                                                                                                 : | :: | : | | : | | | : | | | : | | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
                                                                                                                                                                                                                                                                                                                           DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE--------RH
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ-----
                                                                                                                                                                          :99
Query Match 7.7%; Score 82; DB 5; Length 461; Best Local Similarity 20.4%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : | : | : | : | : | 1: | DGFAAIVSHEITQQILGAYVIGPHASSLIGEMIL----AIRNELT 425
                                                                                                                                                                 69; Indels
                                                                                                                                                                          44; Mismatches
                                                                                                                                                                          Conservative
                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333
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The first in relates to an isolated muchael acid comparising any one or the 6213 antisease sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the acidic cacid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation-required gene or its gene product its corpound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a pene activity; (1) a culture compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (1) a culture compound that inhibits in which the test compound that inhibits in which the cartivity; (1) a culture comprising strains in which the cartivity; (1) a culture comprising strains in which the cartivity; (1) a culture comprising strains in which the cartivity; (1) a culture comprises a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for which each of the strains is present in a culture or collection of strains in proliferation of an organism. The new acute manufact acids are useful for the target prokaryotic essential genes. Note: The sequence data for this cultural directly from WIPO at the present sequence of the target prokaryotic essential genes. Note: The sequence data for this culture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                     Protein encoded by Prokaryotic essential gene #12586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 54983; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107
                                      (revised)
(first entry)
                                                                                                                                                                                      Chlamydophila pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2003-029926/02
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                                                                                                                                                                                                                                 WO200277183-A2.
                                                            19-JUN-2003
                                                                                                                                                                                                                                                                         03-OCT-2002
                                        23-OCT-2003
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Wall D,
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Sequence 461 AA;

ABU27059 standard; protein; 461 AA

RESULT 93 ABU27059 ID ABU2 XX

Query Match

6; Length 461; DB 7.7%; Score 82;

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11;
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                                                                 275
                                                                                          62 VGIV-DFKGELAMRNIEARGLKQMKRQGD-----ANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                                                                                                    333 MDYSAIPSVIFTHP-----EIAMVGLSLQEAEQQNLPAKLTKFPFKAIGKAVALGAS 384
                                         61
                                                      DKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFE-------RH
                                                                                                         114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ-----
                 Gaps
                99
                                                                                                                                                                                                               385 DGFAAIVSHEITQQILGAYVIGPHASSLIGEMTL----AIRNELT 425
                                                                                                                                                                                                --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "wild type Lys replaced by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "wild type Lys replaced by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "wild type Lys replaced by Asn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "wild type Lys replaced by Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "wild type Lys replaced by Glu"
                                                                                                                                                                                                                                                                                                                                                                  Recombinant endotoxin neutralising polypeptide NCY139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "wild type Lys replaced by Asp"
                : 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "wild type Arg replaced
  ed. No. 9;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .31
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                      AAW16827 standard; protein; 487 AA.
                44;
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                Conservative
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                AAW16827;
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17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopaenia, adult respiratory distress syndrome, renal failure, liver disease and conditions associated with Gram negative bacterial ninfection. The RENP has an enhanced serum half life relative to naturally occurring BPI, and binds LPS without triggering a significant, undestrable immune response. N. B. Sequence not given in specification, but produced using the wild type hBPI sequence given in figure 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GIVDFKGELAMRNIEAR------GLKOMKROGDANVKGEEGIVKAHLLIGV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GKPTITCSSCSSHI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Translational profiling, expressed protein tag, BPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; reseptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 HDDI----VSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFA 163
                                                                                                                                                                                                                          The present sequence is the recombinant endotoxin neutralising polypeptide (RENP) B(GAT9) (NCY139), which comprises the human bolypeptide (RENP) B(GAT9) (NCY139), which comprises the human boatericidal/permeability increasing protein (BBP1) mutant Lys148Gly, Lys150Asp, Lys160Asn, Lys161Gln, Arg167Gln, Lys169Val, Lys177Met, Lys185Asp, Lys198Glu. The RENP, which selectively and specifically binds lipopolysaccharide (LPS) and has endotoxin neutralising activity, can be used to detect a site of Gram negative bacterial infection, and prevent or treat endotoxin related disorders, preferably where LPS mediated stimulation of neutrophils and mononuclear cells is inhibited, e.g. shock, disseminated intravascular coagulation, annewna, had an end of the coagulation, annewna, and the coagulation and manemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77
                                                                                      Lipo:polysaccharide binding and endotoxin neutralising polypeptide - useful in diagnosis, prevention and treatment of Gram-negative bacterial infection and associated disorders and conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 VLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKE--LKRIKIFDYSDSFKIKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 G----KGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIAAVAFVAVSADPIHYDKITEE-INKAIDDAIAAIEQSETIDPMKVPDHADKFE-RHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 NVVN-HIGGLSI-----LDPIFGVLSDVLTAIFQDIVRKEMTKVLAPAFK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%; Score 82; DB 2; Length 487; 20.7%; Pred. No. 9.7; ive 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human expressed protein tag (EPT) #1218.
                                                                                                                                                                                     Example 1; Page; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2002; 2002WO-US009671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 20.7%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2003 (first entry)
Scott RW, Marra MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200278524-A2
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ABU04552
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paratrachoma, inclusion conjunctivitis, genital disease, perihepatitis, nongonococcal uretritis, epidymitis, cervicitis, salpingitis, bartholinitis, pneumopathy, venereal lymphogranulomatosis.
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                                                                                                                               W09928475-A2
                                                                                                                                                                                                             27-NOV-1998;
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                                                                                                                                                                         10-JUN-1999
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Matches
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          셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       tragment of a kinase, phosphatase, protesse, protesse inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified ancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and class I or class II MHC-binding polypeptide. The polypeptides and class I or class II MHC-binding polypeptide. The polypeptides and mayeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profiling. Note: This sequence does not appear in the printed from MIPO at the contractive contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIVDFKGELAMRNIEAR------GLKQMKRQGDANVKGEEGIVKAHLLIGV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G----KGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDDI----VSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVROFA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLIAAVAFVAVSADPIHYDKITEE-INKAIDDAIAAIEQSETIDPMKVPDHADKFE-RHV 62
                                                                                                                                                                                                                                                                                                New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 VLVAIGTAVTAAVNPGVVVRISQKGLDYASQQGTAALQKE--LKRIKIPDYSDSFKIKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention describes a purified polypeptide, which comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 NVVN-HIGGLSI-----LDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein involved in intermediate metabolism of nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.7%; Score 82; DB 6; Length 487;
20.7%; Pred. No. 9.7;
ive 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                  New polypeptides (e.g. kinases, phosphatases, cytoskeletal proteins, receptors or transcript
                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 1218; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                    Urban RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY36857 standard; protein; 530
                              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358965P.
                                                                                                                                                                                                                    Towlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 20.7 les 48; Conservative
                                                                                                                                                                                                                                                         WPI; 2003-040607/03
                                                                                                                                                                           (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 487 AA;
                                                                                                                                                                                                                    Chicz RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
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                                                                                                                                                                                                                                                                                                                                                               leukemia
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ZXEXEXEXEX
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122
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY36754-Y17949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, epidymitis, vervicitis, salpingitis, and perihappathis, bartholinitis; pheumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GDYVILHGKLIVYAPRGQYQIVAYALTFSGEGNL-----LQQFEERKQRLAAEGYFDPK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD------IVSMEYDLAYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 NVSLQTSG-------HLYFAIKDSKAVLNGAFFHFRSKYFDRKPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EPLYLQRISYPLYNKSISHN-SHVPMSITSPPIEVSVLTDSIKNLLEKNFLRVVVKGELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GD---LHPTTHVISDIQDF-VVALSLEISDEGNITWISPEVROFANVVNHIGGLSILDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 DPIHYDKITEEI-NKAIDDAIAAIEQSETIDPMKVPDHADK----FERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 82; DB 2; Length 530;
21.6%; Pred. No. 11;
tive 32; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IFGVLSDVLTAIFQDTVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : ||:: | :|
RKKPLPSGARVIGVITSPTGAVIQDILR 182
                                                                                                                                                                                                                                                                                                                                             Genome sequence of Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein sequence SEQ ID NO:14155
                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 731; 1755pp; English
                                                    97FR-00015041.
97FR-00016034.
98US-0107077F.
98WO-IB001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB94022 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                         WPI; 1999-371125/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 530 AA;
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AAB94036;

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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                             Claim 8; SEQ ID NO 14155; 2537pp + Sequence Listing; English.
                                                                                                                              Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                      27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                              28-JUL-2000; 2000EP-00116126.
                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                       Sugiyama
                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                   present invention
 Homo sapiens.
                EP1074617-A2
                                                              29-JUL-1999;
                               07-FEB-2001
                                                                                                                          1 T,
                                                                                                                               Ota T,
Ishii
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Yamamoto J;

Saito K, Ya , Otsuki T,

The present invention describes primer sets for synthesising 5602 fulllength cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonuclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonuclectide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprises a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence of sequence of a combination of the 5'-end sequence 3'-end sequence 15 selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesishing polynucleotides, particularly full-length cDNAs. The primers are also useful for the primers are useful for synthesishing polynucleotides, particularly full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH1363 to AAH1363 and AAH13633 to AAH13631 represent human amino acid sequences; and AAH13629 to AAH1362 represent human amino acid sequences; and AAH13629 to AAH1362 coligonucleotides, all of which are used in the exemplification of the primers are used in the exemplification of the Query Match 7.7%; Score 82; DB 4; Length 767; Best Local Similarity 22.9%; Pred. No. 18; Matches 36; Conservative 30; Mismatches 55; Indels Sequence 767 AA;

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                                             71 LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA------ 119
                                                                                                              600 -----VYPFGIVGMANKGDCLQKGES--VKFQLCV-LGQNAQTWAYNITPLRRATVECVK 651
                          VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHA-DKFERHVGIV---DFKGE 70
                                                                                                                                                    -----YKLGDLHPTTHVISDIQDFVVALSLEISDE 149
                                                                                                                                                                        DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE 685
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600 ----VYPFGIVGMANKGDCLQKGES--VKFQLCV-LGQNAQTMAYNITPLRRATVECVK 651

AAB94036 standard; protein; 767 AA.

RESULT 98 AAB94036 ID AAB9

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The present invention describes primer sets for synthesising 5602 full-

[1] In oligo-dr primer and an oligonucleotide complementary to the

[2] Complementary strand of a polynucleotide complementary to the

[3] Complementary strand of a polynucleotide which comprises one of the 5602

[3] Complementary strand of a polynucleotide which comprises a combination

[3] Complementary strand of a polynucleotide which comprises a 5'-end

[4] Complementary strand of a polynucleotide which comprises a 5'-end

[5] Sequence and an oligonucleotide comprising a sequence complementary to the

[5] Complementary strand of a polynucleotide which comprises a 5'-end

[5] Sequence and an oligonucleotide comprises a 5'-end

[6] Sequence and an oligonucleotide comprises a 5'-end

[7] Sequence and an oligonucleotide comprises a 5'-end

[8] Sequence and an oligonucleotide comprises and an entre sets can be used in antisense therapy and in

[8] Section and/or diagnosis of the abnormality of the proteins encoded by

[8] Complementary strands and sequences; AMH13631 to AMH13632 represent human annino acid sequences; AMH13632 to AMH13632 represent human annino acid sequences; and AMH13632 to AMH13632 represent human annino acid sequences; and AMH13632 to AMH13632 represent human annino acid sequences; and AMH13632 to AMH13632 represent human annino acid sequences; and AMH13632 to AMH13632 represent human entre and the exemplification of the annormal and the exemplification of the anear and annormal and the exemplementary and the annormal and the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHA-DKFERHVGIV---DFKGE
                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; SEQ ID NO 14186; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Length 767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.7%; Score 82; DB
22.9%; Pred. No. 18;
(ve 30; Mismatches
                                                                                                                          Human protein sequence SEQ ID NO:14186.
                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-2000; 2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 767 AA;
                                                                                                                                                                                                                                                                          EP1074617-A2.
                                                                           26-JUN-2001
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---EVROFANV-----VNHIGGLSIL 175

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168 SLELEIIICYLLLDKLIEPHASPKYLIIDEVQDNSVFEFVFALRFAAKHNTSLYLVGDSS 227
                                                     288 ANSF----DAPTADSFKEKVELDMHHV 310
                                                                                      176 DPIFGVLSDVLTA-IFQDTVRKEMTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
N-PSDB; ABL02886.
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                                     152 ITMTSF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 227 AA;
                                                                                                                                                                                                                                                                                                                                        WO200171042-A2
                                                                                                                                                                                                                                                                                        pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions.
                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001;
                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
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                                                                                                                                                                                                    ABB58783;
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Matches
                                                                                                                                                                ABB58783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and analysing a coryneform bacterium. Vitanins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIVDFK-GELAMRN---IEARGL--KQMKRQGDANVKGEEGIVKAHL--LIGVHDDI--V 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 IAVLSFTNAAADNITAKNDKVTSMTISKMVHEIYA------HNFPDHEISTIDTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IAAVAFVAVSADPI--HYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDH-ADKFERHV
                                                                                                                                                                                                                                                                                                                                                                                                                 Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
Senoh A, Ikeda M, Ozaki A;
                                                                                                                                                                                                    bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 17; SEQ ID NO 5445; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 82; DB 4; Length 785; 23.6%; Pred. No. 19; ve 38; Mismatches 80; Indels
                             -----YKLGDLHPTTHVISDIQDFVVALSLEISDE 149
                                                                                                                                                                             C glutamicum protein fragment SEQ ID NO: 5445.
                                                                                                   AAG91691 standard; protein; 785 AA
                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-00127688
                                                                                                                                                                                                                                                                                                                                                     2000JP-00159162
2000JP-00280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.6%;
                                                                                                                                                                                                                                         Corynebacterium glutamicum.
                                                                                                                                                    (first entry)
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03-AUG-2000;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical furugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-BB120707). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                     Sequence 7, Application US/08553336A
Fatent No. 6413738
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: House Dust Mite and Deptides From TITLE OF INVENTION: House Dust Mite and Uses Therefor NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/653,336A
FILING DATE: 22-JUNE-1993
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 38,832
REGISTRATION NUMBER: 38,832
REGISTRATION NUMBER: 38,832
REGISTRATION NUMBER: 38,832
REGISTRATION NUMBER: MIN-032CP2
REGISTRATION NUMBER: MIN-032CP2
REGISTRATION NUMBER: MIN-032CP2
REFERENCE/DOCKET NUMBER: IMI-032CP2
TELEPHONE: (617)22-7400
TELEPHONE: (617)22-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1068; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 213; Conservative 0; Mismatches 0;
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ALIGNMENTS
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-553-336A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                 JS-08-553-336A-7
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US-08-553-336A-2; Sequence 2, Application US/08553336A; Patent No. 6413738

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61 HIGIIDLKGELDMRNIQVRGLKQMKRVGDANVKSEDGVVKAHLLVGVHDDVVSMEYDLAY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMKFLLIAAVAFVAVSADPIHYDKITBEINKAIDDAIAAIBOSETIDPMKVPDHADKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSDKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
APPLICANT: Wayne R. Thomas and Kaw-Yan Chua TITLE OF INVENTION: Allergenic Proteins and Peptides From TITLE OF INVENTION: House Dust Mite and Uses Therefor NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 215;
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| Patent No. 6077517
| GENERAL INFORMATION:
| APPLICANT: Thomas, Wayne R. APPLICANT: Thomas, Wayne R. TITLE OF INVENTION: Allergenic Protein and Peptides From TITLE OF INVENTION: Allergenic Protein and Peptides From TITLE OF INVENTION: Allergenic Protein and Uses Therefor NUMBER OF SEQUENCES: 5
| CORRESPONDENCE ADDRESS: ADDRESSEE: Abhive & Cockfield STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 90.1%; Score 962; DB 4; Length 21 Best Local Similarity 85.9%; Pred. No. 1.9e-101; Matches 183; Conservative 18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
COMPUTER: TEM PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTRICATION NUMBER: US/08/553,336A
FILING DATE: 10-UNN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/081,540
FILING DATE: 22-JUNE-1993
ATTONEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 1MI-032CP2
TELEPHONE: (617)227-7400
TELEFPAX: (617)227-7401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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RESULT 5
US-08-336-618-12
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; Sequence 8, Application US/08973462B
; Patent No. 6191270
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; CURRENT FILING DATE: 1998-02-06
; EARLIER FILING DATE: 1998-06-12
; EARLIER FILING DATE: 1996-06-12
; EARLIER FILING DATE: 1996-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFFWARE: PATENTIN VOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MMKFLLIAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.8%; Score 959; DB 3; Length 215; Best Local Similarity 85.4%; Pred. No. 4.1e-101; Matches 182; Conservative 19; Mismatches 12; Indels
                                                                                                                                                                                                CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/031,141

FILING DATE: 12 March 1993
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-053CP (IMI-032CP)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-227-7400
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,778
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEKN 213
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ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 215 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                617-227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
USA
COUNTRY: U
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APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN ME 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              82 KOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIODFVVA 141
                                                                                                                                                                                                                                                                                                                                                                                                               142 LSLEISDEGNITMISFEV----RQFANVVNHIGGLS----ILDPIFGVLSDVLTA--IFQ 191
                                                                                                                                                                                                22 YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGL 81
                                                                                                                                                Gaps
; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
US-08-973-462-8
                                                                                    Query Match

8.4%; Score 90; DB 3; Length 1786;
Best Local Similarity 23.3%; Pred. No. 1;
Matches 47; Conservative 43; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Hamilton, Brook, Smith and Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1993
APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-OCT-1991
PROOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 10-OCT-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1136 EPVOKEVEKETVSIIE-EMEEN 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 DIVRKEMTKVLAPAFKRELEKN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08336618
Patent No. 5763590
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGIETRATION NUMBER: 32,22
REPERENCE/DOCKET NUMBER: V
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 459 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 32 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
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17; Gaps

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75 DKFSFDLGKGEVIKAWDIAIATMKVGEVCHITCKPEYAYGSAGSPPKIPPNATLVFE--V 132
                                                                                                                                                                                                 63 GIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKL 122
                                                                                                                                                                                                                                           78 IAMEEADVIVEVVSGKEGITDADEYVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AN-----SMEYDL----AHLLIGVHDDIV-----SMEYDL----AYK 121
                                                                      -- DPMKVPDHAD-KFERHV 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 8.2%; Score 88; DB 4; Length 393;
Best Local Similarity 21.8%; Pred. No. 0.17;
Matches 46; Conservative 34; Mismatches 89; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09393858;
Patent No. 6627747;
GENERAL INFORMATION:
APPLICANT: Fritz, Christian
APPLICANT: Garman, Philip
APPLICANT: Garman, Luz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 06266-080001
CURRENT APPLICATION NUMBER: US/09/393,858
CURRENT PRILIG DATE: 1999-09-09;
PRIOR PRILICATION NUMBER: 60/099,578
PRIOR FILING DATE: 1998-09-09;
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09393858

Patent No. 6627447

GENERAL INFORMATION:
APPLICANT: Fritz, Christian
APPLICANT: Fritz, Christian
APPLICANT: Graman, Philip
APPLICANT: Graman, Luz-Maria
TITLE OF INVENTION: ESSENTTAL BACTERIAL GENES AND THEIR USE
FILE REFREENCE: 06286-088001
CURRENT FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 06/099,578
PRIOR APPLICATION NUMBER: 60/099,578
PRIOR APPLICATION NUMBER: 60/099,578

PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 4.0
       Indels
   50;
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       25; Mismatches
                                                                      18 DPIHYDKITEEINKAIDDAIAAIEQSETI-
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          Conservative
                                                                                                                                                                                                                                                                                                                                                                                 |:
GE 194
                                                                                                                                                                                                                                                                                                                                   GD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Peattie, Debra A.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: PROTEIN AND MOLECULAR CLONING OF A CORRESPONDING HUMAN
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                             63 GIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKL 122
                                                                                                                                                                                                                                    18 DPIHYDKITEEINKAIDDAIAAIEQSETI------DPMKVPDHAD-KFERHV
                                                                                                                                                                     17;
                                                                                                  Query Match 8.3%; Score 88.5; DB 1; Length 459; Best Local Similarity 24.6%; Pred. No. 0.19; Matches 30; Conservative 25; Mismatches 50; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.3%; Score 88.5; DB 1; Length 459; 24.6%; Pred. No. 0.19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1992
ATTOMEY/AGENT INFORMATION:
AND APPLICATION NUMBER: PCT/
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ATTOMET/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGENT/AGE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5763590
GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: VPI9:
TELEPHONE: 617-861-6240
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           459 amino acids
amino acid
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MOLECULE TYPE: protein
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Best Local Similarity
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          ; MOLECULE 11:
US-08-336-618-12
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US-08-336-618-26
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9, Application US/08137175A
Sequence 9, Application Patent No. 5777095 GENERAL INFORMATION:
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Patent No. 6551795
GENERAL INFORMATION:
PAPELICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 MKRQGDANVKGEEGIVKAHLLIGV-----HDDIVSMEYDLAYKLGDLHPTTHVISDIQ 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGD 89
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                     Query Match
8.2%; Score 88; DB 4; Length 436;
Best Local Similarity 21.8%; Pred. No. 0.2;
Matches 46; Conservative 34; Mismatches 89; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 DRVIASPVAĞTTRDAIDTHFTDTDGQEFTMI 228
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                           i LENGTH: 436
i TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-393-858-5
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ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-22392
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RESULT 10 US-08-137-175A-9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LIGVHDDI--VSME-YD-----LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGN 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
APPLICANT: BARBOUR, Alan G.
APPLICANT: BERGSTROEM, Sven
APPLICANT: HANSSOW, Lennart
ITILE OF INVENTION: IMPROVEMENT IN BORRELIA BURGDORFERI AND
TITLE OF INVENTION: PROPHYLAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATE: US/08/137,175A FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MMKFLL----IAAVAFVAVSADPIHYDKITEEINK---
                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STRRET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.9%; Score 84.5; DB
Best Local Similarity 22.3%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 26-OCT-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08479017
Patent No. 6143872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BA
TELECOMOUNICATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BARBOUR, Alan G. APPLICANT: BERGSTROEM, Sven APPLICANT: HANSSON, Lennart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 294 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COOPER, Iver P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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US-05-498-520A-34

US-07-498-520A-34

Sequence 34, Application US/09498520A

Sequence 34, Application US/09498520A

Sequence 34, Application US/09498520A

GENERAL INFORMATION:
APPLICANT: Rock, Charles O

TILLE OF INVENTION: No. 6613553el Enoyl Reductases and Methods of Use Thereof
FILE REFERENCE: SJ-0022

CURRENT APPLICATION NUMBER: US/09/498,520A

CURRENT PILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 62

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 MRNIE-ARGL-KOMKROGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                      121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 T----THVISDIQDFVVALSLEISD-----EGNITMISFEVROFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 DSLARMVERAGADĀVIAEGMESGGHĪGEVTTFVLVNKVSRSVNIPVIAAGGĪADGRĞMAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 MRNIEARGLKOMKR-----QGDANVKGEBGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHP 127
                                                                                                                                                                                                                                                                                            18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 ARVLRTPFARKIQEMEFENPMQAEEMLVGSLRRAVVEGDLERGSFMVQQSAGLIDEI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - - GIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Gaps
                                                                                                                                                                                                            7.9%; Score 84.5; DB 4; Length 823; 23.0%; Pred. No. 1.4; tive 35; Mismatches 87; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.9%; Score 84; DB 4; Length 314; Best Local Similarity 23.5%; Pred. No. 0.35; Matches 48; Conservative 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DKITEEINKAIDDAIAA--IEQSETIDPMKVPDHADKFERHV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/055,779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Thermotoga maritima
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US EPRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4081
                                                                                                                                                                                                                              Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-673-395A-197
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LENGTH: 314
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                                                                                                                                                                                                                 Query Match
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Patent No. 6380370

GRERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 LIGVHDDI--VSME-YD-----LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPROVEMENT IN BORRELIA BURGDORFERI AND PROPHYLAXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MMKFLL----IAAVAFVAVSADPIHYDKITEEINK---
                                                                                   ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 84.5; DB 22.3%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,175
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: BARBOUR=1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   294 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.3%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                         NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY ANI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-134-001C-4081
                                                                                                                                                                                      20004
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TOPOLOGY:
                                                                                                                                                                     COUNTRY:
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uccette-Stamm and David Bush
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 EGDGHALNHVSLTFPAASMSALVGASGAGKTTVTKLLMR-YADPQQGQISIGGVDIRRLT 462
             122 LGDLHPTTHVISDIQDFVVALSLEISDEGNITWTSFEVRQFANVVN---HIGGLSILDPI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 EEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 83; DB 4; Length 583;
18.7%; Pred. No. 1.2;
tive 36; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: JUNY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 5678:
US-09-107-532A-5678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococus faecium
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                     RESULT 16
US-09-107-532A-5678
; Sequence 5678, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5678:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                               |: ::: :|||
463 PEQLNSLISVVFQD 476
                                                                                                                  179 FGVLSDVLTAIFQD 192
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Best Local Similarity 18.7%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
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Benent No. 6610836

GENERAL INFORMATION

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1095-01-29

NUMBER OF SEQIEN NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE-----VEFSVIFKSSGGL 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VGIVDFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYK 121
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                                         APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, THOMAS
APPLICANT: HINZMANN, BERND
APPLICANT: BILARKY, CHRISTIAN
APPLICANT: PLIARKY, CHRISTIAN
APPLICANT: BLAGKY, CHRISTIAN
APPLICANT: DAHL, EDGAR
APPLICANT: ROSENTHAL, ANDRE
TITLE OF INYENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT APPLICATION NUMBER: 2000-10-17
NUMBER OF SEQ ID NOS: 637
SOFTWARE: PATENT NOS: 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 VSAEKVNK---THSVNGITEEADPTIYSGKVIRPLRSVDPTQTEYQGMIEIVEEGDMKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LAMRNIBARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.9%; Score 84; DB 4; Length 410; 22.1%; Pred. No. 0.53; tive 33; Mismatches 62; Indels
Sequence 197, Application US/09673395A
Patent No. 6620923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Klebsiella pneumoniae
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Best Local Similarity 22.1%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-673-395A-197
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US-09-489-039A-14142
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LENGTH: 649
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CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                   TYPE: PRT ORGANISM: Leishmania major
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                                                                   SEQ ID NO 110
LENGTH: 845
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                            164 TQMLFAHHGLTLRDKK--APSVFFVKKLKNTLNHVYGYAVL----SISSKQLANLFOSVV 217
135 IQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL-----RQALTERIRP 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VNFTVDQVRELMDYPDQIRNMSVIAHVD------HGKSTLSDSLVGAAGIIKMEEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 EISDEGNITMTSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS FILE REFERENCE: 210121.420c6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COLEY, Rhea APPLICANT: COLEY, Rhea APPLICANT: Probst, Peter TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS FILE REFERENCE: 210121.420C7
CURRENT APPLICATION NUMBER: US/09/639,206A
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7.8%; Score 83; DB 4;
Best Local Similarity 23.3%; Pred. No. 2.1;
Matches 42; Conservative 34; Mismatches 70
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COCATION: (1)...(845)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-565-501A-110
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                                                                                                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Peter Probst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
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ORGANISM: Leishmania major
                                                                                      195 RKEMTKV 201
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218 NPEISKI 224
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APPLICANT: Reed, S
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US-09-565-501A-110
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US-09-639-206A-110
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Dialion, Davin C.
APPLICANT: Blatia, Ajay
APPLICANT: Blatia, Ajay
APPLICANT: Brain, Mark
APPLICANT: Probst, Peter
APPLICANT: Probst, Peter
APPLICANT: Tribe OF INVENTION: LISTANANA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LISTANANA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: LISTANANA AND DIAGNOSIS OF LEISHWANIASIS
FILE REFERENCE: 210121.420C8
CURRENT APPLICANION NUMBER: US/09/874,923
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
                                                                                                                                                                              Query Match 7.8%; Score 83; DB 4; Length 845; Best Local Similarity 23.3%; Pred. No. 2.1; Matches 42; Conservative 34; Mismatches 70; Indels
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FEATURE:

NAME/ERT:

LOCATION: (1)...(845)

OTHER INFORMATION: Xaa = Any Amino Acid
US-09-639-206A-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATTON: (1)...(845)
COTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-110
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269 MDYSAIPSVIFTHP-----EIAMVGLSLQEAEQQNLPAKLTKFPFKAIGKAVALGAS 320
212 AGVIRDDRGVIPVDETMRTNVPNIYAIGDITGKWLLAHVASHQGVIAAKNISGHHB---V 268
                                                                  114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNI--TMTSFEVRQ-
                                                                                                                                                                                                   --FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
                                                                                                                                                                                                                                                 APPLICANT: Young, Richard A. and Young, Douglas TITLE OF INVENTION: Stress Proteins and Uses Therefor NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tall PC Compatible
COMPTUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FLING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION NUMBER: 08/336,251
FILING DATE: 06-JUN-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 06-JUN-1994
CLASSIFICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION NUMBER: US 07/804,632
FRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/306,581
FILING DATE: 10-JUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                       US-08-461-722-2; Sequence 2. Application US/08461722; Sequence 2. Application US/08461722; Patent No. 6335183; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        547 amino acids
amino acid
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STATE: MA
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Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering PILE REPERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ. ID NOS: 6849
                                                                                                                                                                                                                 Sequence 4057, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR PEDICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-01-4

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 4657

LENGTH: 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VGIV-DFKGELAMRNIEARGLKQMKRQCD-----ANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 MKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT-THVISDIQDFVVAL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SLEISDEGNITWISFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 AQQY--HAHVITTDFNL----NKVCHVQGITALN-----VNDLSEAIKPNVHQGDQLSIL 306
                                                    145 BISDEGNITMISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMIKVLAP 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39; Indels
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7.7%; Score 82; DB 4
Best Local Similarity 24.4%; Pred. No. 0.74;
Matches 31; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4057
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US-09-134-001C-4057
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US-09-198-452A-894
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72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
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                                                                                                                                                                                                                                                                                                                                                        13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 FANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
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                                                                                                                                                                                                            7.6%; Score 81.5; DB 4; Length 547; 20.4%; Pred. No. 1.6; trive 37; Mismatches 85; Indels 65
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| Sequence 2, Application US/09468041
| Patent No. 6482614
| GENERAL INFORMATION:
| APPLICANT: Young, Richard S. APPLICANT: Young, Richard S. APPLICANT: Young, Richard S. APPLICANT: Young, Richard S. APPLICANT: APPLICANT: APPLESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Allitia Drive
| CITY: Lexington | CITY: Lexington | CITY: Lexington | CITY: Lexington | CITY: Lexington | CITY: Control | CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRATION DATA:
APPLICATION NUMBER: US/09/468,041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-UN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-UN-1989
ATTORNEY/AGENT INPORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-UNW-1993
CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
                 547 amino acids
                                                                                                                                                                                                                                                    Best Local Similarity 20.4%
Matches 48; Conservative
                                              ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-336-251-2
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                 LENGTH:
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                                                                                                                                    13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 FANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
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              DB 4; Length 547;
                                                                           Indels
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APPLICANT: Young, Richard S.
TITLE OF INVENTION: Stress Proteins and Uses Therefor NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Rolease #1.0, Version #1.25
APPLICATION NUMBER: US/08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/05362
FILING DATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/0/3,381
FILING DATE: 04-JUN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/0/84,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0/20,298
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0/20,298
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: LS-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
   ch 7.6%; Score 81.5; D Similarity 20.4%; Pred. No. 1.6; 48; Conservative 37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 23
US-008-336-251-2
Bequence 2, Application US/08336251
Patent No. 6338952
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-6240 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Query Match
Best Local S
Matches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 ---VVNTIRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEEIGWELEK 311
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                                                                                                                                                                                                                                                                             85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Stress Proteins and Uses Therefor NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTUMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-UNN-1994
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: 2 Militia Drive CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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7.6%; Score 81.5; DE
Best Local Similarity 20.4%; Pred. No. 1.6;
Matches 48; Conservative 37; Mismatches
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA3
TELECOMMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 PTTHVISDIQDFVVALSLEISD------
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APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-UTN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9406362 GENERAL INFORMATION:
                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 547 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 amino acids
amino acid
                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-468-041-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein PCT-US94-06362-2
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PCT-US94-06362-2
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APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INPECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE Finnegan, Henderson, Farabow, Garrett &
                                                                                                             72 AMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
                                                                                                                                                                                                      127 PTTHVISDIQDFVVALSLEISD---------EGNITMISFEVRQ 161
                                                                                                                                                                                                                                                                                                 13 VAVSADPIHYDKITEEINKAIDDAI-AAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
                                                                                                                                                                                                                                                                                                                                                    162 FANVONHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                              263 ---VVNTIRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEEIGMELEK 311
Query Match 7.6%; Score 81.5; DB 5; Length 547; Best Local Similarity 20.4%; Pred. No. 1.6; Matches 48; Conservative 37; Mismatches 85; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03495.0137-02000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFRENCE/DOCKET NUMBER: 03495
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 548 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero. Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICODBACTER INPECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                              ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                     Finnegan, Henderson, Farabow, Garrett
Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAVE: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 03495.0137-00000
TELECCOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.6%; Score 81.5; DE 20.4%; Pred. No. 1.6; Live 37; Mismatches
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
TVPD
TVPD
TVPD
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Best Local Similarity
Matches 48; Conserv
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STREET: 13
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                                                                                                                                                                                                                                                                                                                                     PTHVISDIQDFVVALSLEISD--------EGNITWISFEVRQ 161
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                                                                                                                                                                                                                                                                            157 TVGKLIAEAMDKV------GKEGVITVEDGTGLQDELDVVEGMQFDRGYLSPYFINK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%; Score 81.5; DB 3; Length 548; 20.4%; Pred. No. 1.6; ive 37; Mismatches 85; Indels 6
                                                                                   DB 2; Length 548;
                                                                                                                           85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YANGI, Hideki
APPLICANT: YANGI, Hideki
APPLICANT: YANGI, Hideki
APPLICANT: YANGI, Hideki
APPLICANT: YARA, TARASHI,
TITLE OF INVENTION: TRIGGER FACTOR EXPRESSION PLASMIDS
FILE REFERENCE: 1422-409P
CURRENT FALING DATE: 1999-12-28
EARLIER APPLICATION NUMBER: UP10-372965
EARLIER FILING DATE: 1998-12-28
MUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHIN VOI: 2.1
SEQ ID NO 3
                                                                               7.6%; Score 81.5; Di
20.4%; Pred. No. 1.6;
tive 37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09472971
Patent No. 6197547
GENERAL INFORMATION:
                                                                                 Query Match
Best Local Similarity 20.4%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-472-971-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Conservative
; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-467-822-32
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Best Local Similarity
Matches 48; Conserv
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US-08-432-697-32
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US-09-472-971-3
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72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAYKLGDL--H 126
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                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 548;
                                         Indels
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Patent No. 6258359
GENERAL INFORMATION.
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Freerero, Richard L.
APPLICANT: Thiberge, Jean-Wichel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
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59 BRHVGIVDFKGELAMRNIE--ARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 -----ALAIQAIKLIANNLRQAVALGE-NLEARENMAYASLLAGMAFNNANLGY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 --DLAYKLGDLHPTTHVISDIODFVVALSLEISDEGNITMTSFEVROFANVVNHIG---- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MKFLLIAAVAFVAVSA-DPIHYDKITEEINKA--IDDAIAAIEOSETIDPMKVPDHADKF
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                                   APPLICANT: Selifonova, Olga V.
TITLE OF INVENTION: Mutant 1,3-Propanediol Dehydrogenase
FILE REFERENCE: GCS 800-2
CURRENT APPLICATION NUMBER: US/09/570,778A
CURRENT FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: US 60/134,868
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.6%; Score 81; DB 23.8%; Pred. No. 1.1; tive 39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ; ORGANISM: Clostridium pasteurianum US-09-570-778A-12
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Matches 48; Conservative
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Matches 48; Conserve
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US-09-991-138-12
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HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 FANVVNHIGGL----SILDPIFGVLSDVLTAIPODTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---VVNTIRGIVKVAAVKAPGFG---DRRKAMLQDIATLIGGTVISEEIGMELEK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: PLOBY disk
CONTUTER: IBM PC compatible
CONTUTES: IBM PC compatible
CONTUTES: IBM PC compatible
CONTUTES: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION 435
PRIOR APPLICATION WHERE: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: US 0495.0137-02000
TELEPOMUNICATION INFORMATION:
NAME: MAYERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 25,146
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REGISTRATION NUMBER: 25,146
REGISTRATION NUMB
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 20.4:
Matches 48; Conservative
                              TITLE OF INVENTION: HELL TITLE OF INVENTION: COMP TITLE OF INVENTION: POLY NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
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117 --DLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIG---- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 MKFLLIAAVAFVAVSA-DPIHYDKITEEINKA--IDDAIAAIEQSETIDPMKVPDHADKF 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/0999138
Patent No. 655893
GENERAL INFORMATION:
APPLICANT: Trimbur, Donald E.
APPLICANT: Trimbur, Donald E.
APPLICANT: Whited, Gregory M.
APPLICANT: Selifonova, Olga V.
TITLE OF INVENTION: Mutant I. 3-Propanediol Dehydrogenase
TILE REFERENCE: GC580-2D1
CURRENT APPLICATION NUMBER: US/09/991,138
CURRENT FILING DATE: 2001-11-16
PRIOR PRILING DATE: 2000-05-19
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 81; DB 4; Length 385;
23.8%; Pred. No. 1.1;
ive 39; Mismatches 71; Indels
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Sequence 12, Application US/09570778A
Patent No. 6468773
GENERAL INFORMATION:
APPLICANT: Trimbur, Donald E.
APPLICANT: Whited, Gregory M.

RESULT 30 US-09-570-778A-12

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APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REBRENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-507
INFORMATION FOR SEQ ID NO: 4950:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4950:
US-09-107-532A-4950
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                         LENGTH: 255 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-8512
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                       APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, THOMAS
APPLICANT: SPECHT, ARMIN
APPLICANT: SCHMIT, ARMIN
APPLICANT: SCHMIT, ARMIN
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
APPLICANT: DAHL, EDGAR
TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
FILE REFERENCE: ALBRE-12
CURRENT APPLICATION NUMBER: US/09/673,395A
CURRENT APPLICATION NUMBER: US/09/673,295A
SOFTWARE: PATENTING OFF: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 VSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHAD-KFERHVGIV---DFKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 LAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 81; DB 4; Length 470; 22.9%; Pred. No. 1.4; tive 29; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
COMPUTER: PC
COMPANDED SYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4950, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                      171 GLSI-----LDPIFGVLSDV 185
                                                                                              |||: ||: || ||315 GLSVMEAAEKAIDAMFRLSKDV 336
                                                                                                                                                                                                              Sequence 561, Application US/09673395A Patent No. 6620923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-673-395A-561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                           RESULT 32
US-09-673-395A-561
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Sequence 8512. Application US/09489039A

Patent No. 6610836

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: GATY BRETON et. al

APPLICANT: CATY BRETON ENCLIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

FILE REPERSONCE: 2709.2004001

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 NDKLYNRMDAEDFKKCLDINLIGTFNWTQHVLKKWMKQREGAIINLSSVSGLIGNIGQAN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY----- 120
                                                                                                                                                                                                                                                                                                                            ----VKGEEGIVKAHLLI---GVH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 DDIVSMEYDLA-YK-----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 FEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 YAASK-AGVVGLTKSVAREAATRGITCNAIAPGF---ITTDMTEVLADKVKEQAEK 214
                                                                                                                                                         31; Gaps
        DB 4; Length 255;
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Query Match 7.5%; Score 80.5; DB Best Local Similarity 23.3%; Pred. No. 0.64; Matches 41; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                            64 IVDFKGEL---AMRNIEARGLKOMKROGDAN----
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Query Match 7.5%; Score 80; DB 4 Best Local Similarity 21.1%; Pred. No. 11; Matches 39; Conservative 30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 VLTAIFODTVRKEMTKVLAPAFKRELE 211
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Sequence 10, Application US/09561818A
Patent No. 6638907
GENERAL INPORMATION:
APPLICANT: Kortesmaa, Jarrko
      ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-12
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Best Local Similarity
Matches 44; Conserva
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APPLICANT: Marc J. Rubenfield et al,
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ADERGEN US.
FILE REFERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US. 60/074, 788
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26608, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION
ADDITIONATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TUTLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26608
LENGTH: 1504
                                                                  212 PDTGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLVIIAEDVEGEALATL---- 266
                                          ----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
---GKEGVITVEDGTGLEDELDVVEGMQFDRGYLSPYFINK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAMRN----IEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 LILQDQVEFLQRRGLHGVQR-GDA----QDDIQAHLVV------ENAEHLGGL- 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 PTTHVISDIQDFVVALSLEISDEGNITMISFEVRQFANVVNHIGGLSILDPIFGVLSDVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------VTDHVGHGTRLHPLQAVQA-AG 312
                                                                                                                    160 RQFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                         73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ADPIH---YD---KITEZINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 538;
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Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
  161 TVGKLIAEAMDKV--
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US-09-252-991A-26608
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100 ------KAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEI 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 TLESELDEIIKNASGI-----YAEIDGAKNELQCKLSNLSNLSHDLVQEATDHAYNL 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 ------SLEISDEGNITMISFEVRQ-FANVVNHIG------GLSILDPIFGVLSD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              567 QQEADELSRNIHSSDMNGLVQKALDASNVYENIANYVSEANETAELALNITDRIYDAVSG 626
                                                                                                                                                                                                               66 DFKGEL-----EEGIV----99
                                                                                                                                                                                                                                                     6 LIAAVAFVAVSADPIHYDKITEBINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIV
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                                                       70;
DB 4; Length 1504;
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                                                    46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09561818A
Patent No. 6638907
GENERAL INFORMATION:
APPLICANT: Kortesmae, Jarrko
APPLICANT: Kortesmae, Jarrko
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
TITLE OF INVENTION: Laminin 8 and Methods For Its Use
CURRENT APPLICATION NUMBER: US/09/561,818A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 1792
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TITLE OF INVENTION: Laminin 8 and Methods For Its Use
FILE REFERENCE: 99,274-D
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acidi
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US-09-543-681A-6606
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US-08-094-889-1
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APPLICANT: Parting, Matthew W.
APPLICANT: Harding, Matthew W.
APPLICANT: Livingston, David J.
TITLE OF INVENTION: ISOLATION OF AN Mr 52,000 FK506 BINDING
TITLE OF INVENTION: ISOLATION OF AN MC 52,000 FK506 BINDING HUMAN
TITLE OF INVENTION: ODNA
TOTHE OF INVENTION: CDNA
OUTBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                    34; Gaps
                                                                                                                                                                                                             DB 4; Length 1816;
                                                                                                                                                                                                                                                       90; Indels
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STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,618
FILING DATE: 09-NOV-1994
CLASSIFICATION NUMBER: 07/963,325
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/777,752
APPLICATION NUMBER: US 07/777,752
                                                                                                                                                                                                             Query Match
7.5%; Score 80; DB 4
Best Local Similarity 21.3%; Pred. No. 15;
Matches 44; Conservative 39; Mismatches
  CURRENT APPLICATION NUMBER: US/09/561,818A CURRENT FILING DATE: 2000-04-28 NUMBER OF SEQ ID NOS: 28 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 VLTAIFODTVRKEMTKVLAPAFKRELE 211
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APPLICATION NUMBER: US 07/777,752
FILING DATE: 11-0CT-1991
APPLICATION NUMBER: PCT/
FILING DATE: 09-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: VP191-06A
TELEPHONE: 617-861-6240
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Massachusetts
                                                                                                                            TYPE: PRT
CRGANISM: Mus musculus
US-09-561-818A-10
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                                                                                                             LENGTH: 1816
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Sequence 6606, Application US/09543681A

Sequence 6606, Application US/09543681A

Parent NO. 66057AD

GREEAT NO. 66057AD

TITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL1

TITLE OF INVENTION: UCCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 VAVSADPIHYDKITEEINKAIDDA-IAAIEQSETIDPWKVPDHADKFERHVGIVDFKGEL
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                                                                                                                                                            7.4%; Score 79.5; DB 1; Length 458; 22.1%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                                                 49;
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7.4%; Score 79.5; DE
Best Local Similarity 17.7%; Pred. No. 2.8;
Matches 42; Conservative 46; Mismatches
                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                          18 DPIHYDKITEEINKAIDDAIAAIEQSETI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08094889
Patent No. 8470866
GENERAL INFORMATION:
APPLICANT: Shinji HIRANO et al.
24:
    , ORGANISM: Proteus mirabilis
US-09-543-681A-6606
                                                                                                                                                                       Ouery Match
Best Local Similarity 22.1%
Matches 27; Conservative
                                                                                                     , MOLECULE TYPE: protein US-08-336-618-24
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us-10-024-955-7.rai

US-08-094-889-1

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STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER: EDAGELE FORM:
MEDLUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,889
FILING DATE: U1/2 2, 1993
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATORNEY/AGENT INFORMATION:
NAME: WATEN M Check, Jr.
RECISTRATION NUMBER: 33.367
REFERENCE/DOCKET NUMBER:
TELEPPHONE: 202-371-8850
                                                   ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
     NEURAL '-CATENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 906 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KRY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE OF INVENTION: NE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
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RESULT 42

US-09-522-991A-27391

i gequence 27391, Application US/09252991A

i patent No. 6551795

i GENERAL INFORMATION:

i TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PRIOR REPERRORE:

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR PEDITCATION NUMBER: US 60/074,788

PRIOR PEDITCATION NUMBER: US 60/074,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 400
                                           10;
                                                                                                   88 GDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEIS 147
                                                                                                                                                                                                                                                                                                   148 DEGNITMISFEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLA---- 203
                                                                                                                                                                                                                                                                                                                             ----YDLAYKLGDLHPTTH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 VISDIQD-----FVVALSLEISDEG--NITWISFEVRQFANVVNHIGGLSILDPIFGVL 182
                                                                           18 DPIH--YDKITE------EINKAIDDAIA------AIEQSETIDPMKVPDHAD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 ITEEINKAIDDAIAAIE-QSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQ 83
                                                                                                                                                 57 KFERHVG-IVDFKGELAMRNIBARGLKQMK-----RQ
                                         71; Gaps
Query Match
7.4%; Score 79.5; DB 1; Length 906;
Best Local Similarity 19.4%; Pred. No. 5.8;
Matches 48; Conservative 47; Mismatches 82; Indels 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
7.4%; Score 79; DB 4; Length 400;
Best Local Similarity 20.4%; Pred. No. 1.9;
Matches 43; Conservative 46; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 MKRQGDANVKGEEGIVKAHLLIGVHDDIVSME-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 --SDVLTAIFQDTVRKEMTKVLAPAFKRELE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 43
US-09-252-991A-32411
; Sequence 32411, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27391
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584 PRFAEQVE 591
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Matches
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Sequence 6150, Application US/09134000C
Sequence 6150, Application US/09134000C
Sequence 6150, Application US/09134000C
SEXERAL INFORMATION:
CENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BATEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERBNOE: 032796-032
CURRENT PAPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1999-08-13
PRIOR FILING DATE: 1997-08-15
                                                                                Sequence 3522, Application US/09134000C

Batent No. 6647156
GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn DOUCETTE-STAMM et al
APPLICANT: Lynn DOUCETTE-STAMM et al
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 02796-03
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
RRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PETENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 EGIVKAHLL -----IGVH--DDIVSMEYDLAYKLGDLHPTTHVISDI-QDFVVALSLFI 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 LLIAAVAFVAVSADPIHYDKITEEINKAIDDALAAIEQSETIDPMKVPDHADKFERHVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AAIEQSETIDPMKVPDHADKFE--RHVGIVDFKGELAWRNIEARGLKQMKRQGDANVKGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 AAIAKKETL----VQAAAEKFESAASVVIVDYRG---LTVEEVTNLRKQLR--DAGV--E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.4%; Score 78.5; DB 4; Length 437; 21.7%; Pred. No. 2.5; tive 38; Mismatches 85; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 78.5; DB 4; Length 166; 28.4%; Pred. No. 0.56; tive 30; Mismatches 61; Indels 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21.7%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 KGGVIĖĠKVSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 YAVKAVAĖKN 162
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Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 46
US-09-134-000C-6150
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                                                                            US-09-134-000C-3522
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LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3522
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ORGANISM:
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APPLICANT:
MARC J. RUBEnfield et al.
APPLICANT:
MARC J. RUBEnfield et al.
APPLICANT:
MARC J. RUBEnfield et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23008
LENGTH: 768
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,786
PRIOR PLILNG DATE: 1999-02-18
PRIOR PLILNG DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ERGOTH: 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| ::: :: | | | : | | :: | :| | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | | :: | | | | :: | | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | | :: | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 AAVEQAGAGEQFVVPDGFFLEVGPVAGGQVERHAPGVVAAADQAADGPVRGRG----EGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 AAIEQSETIDPMKVPD------HADKFERHV-GIVDFKGELAMRNIEARGLKQMKRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4%; Score 79; DB 4; Length 593; 23.6%; Pred. No. 3.5; tive 25; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 LSLEISDEGNITMTSFEVROFANVVNHIG-GLSILDF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 AVVQLAEHTEVLLRVVEGRQPAQVQCLVGAGAGVVDP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.4%; Score 79; DB 4 Best Local Similarity 23.6%; Pred. No. 5.1; Matches 35; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 IFGVLSDVLTAIFQDTVRKEMTKVLAPA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      682 VVGLVVRAQAGLGDDAVENVVFAVLVPA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Sequence 23008, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.6%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 44
US-09-252-991A-23008
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121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMISFEVRQFANVV----NHIGGL 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 MRNIB-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                 | | : :: | | : :: | 463 K----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIMISNVGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 DPIHYDKITEE----INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                     173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                 7.4%; Score 78.5; Di 22.6%; Pred. No. 4.8; tive 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-311-2000
FILING DATE: 4-311-2000
PRIOR APPLICATION AND AND AND APPLICATION NUMBER: 09/040,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Fall, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & STREET: 4000 Bell Atlantic CITY: Philadelphia
                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09621855
Patent No. 6346608
GENERAL IRPORMATION:
APPLICANT: Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                Wang, Min
Shilling, Lisa K.
Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hodgson, John E.
Lawlor, Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Posberry, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ward, Judith
TITLE OF INVENTION: MecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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Matches 49; Conserva
                                                                                                                                                                                                                                                                               US-09-621-855-4
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                                  133 QIDAFYIADY------TRIQRQVNSIIKEEBYLALQHL-----TRTRYQ 170
                                                                                                                                                              161 OPANVVNHIGGLSILDP--IFGVLSDVLTA-----IFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                          64 -----IVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
                                                                                                                     171 LIKQL - VRTKQHFİENİYYKCNTLSKELKAEĞGSVLSATLVTLMTEDYTMDQLAELSLE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 MRNIE-ARGL-KQMKRQGDANVKGE-EGIVKAHL---LIGV-----HDDIVSMEYDLAY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLHERVIGOKDAVNSISKAVRRARAGLK----DP------KRPIGSFIFLGPTG 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 DPIHYDKITEE----INKAIDDALAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 672;
                                                                                LAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Dechert, Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
SOFTWARE: FRSTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.4%; Score 78.5;
Best Local Similarity 22.6%; Pred. No. 4.
Matches 49; Conservative 37; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/057,535
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REJESTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM10082
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GM10082
                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09040843
Patent No. 6124119
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        Jaworski, Deborah J.
                                                                                                                                                                                                                                                                                                                                                                                         Wang, Min
Shilling, Lisa K.
Burnham, Martin
Fosberry, Andrew
Hodgson, John E.
Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: CL. 2793
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

~~METTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosenbérg, Martin
APPLICANT: Ward, Judith
TITLE OF INVENTION: MeCB
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 672 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 4000 Bell A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                  RESULT 47
US-09-040-843-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
                                                       121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMISFEVRQFANVV----NHIGGL 172
                                                                                            504 DILHERVICOKDAVNSISKAVRRARAGLK-----DP-----KRPIGSFIFLGPTG
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549 VGKTELARALAESMFGDDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPATING SYSTEM: Windows 95
SOFTWARE: FRSTSEQ for Windows Version 2.0b
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/621,855
FILING DATE: 24-U11-2000
CLASSIFICATION: <university Company (CLASSIFICATION: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classification: <university Classification: <university Classification: <university Classification: <ul>CLASSIFICATION: <university Classification: <university Classifi
                                                                                                                                                                            173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 78.5; DB 22.6%; Pred. No. 7; Live 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/040,843
FILING DATE: -Unknown>
ATTORNEY/AGENT INPORMATION:
NAME: Fell., Stephen T
REGISTRATION NUMBER: 36,795
REPERENCE/DOCKET NUMBER: GM10082
TELECHONNINICATION INPORMATION:
TELEPHONE: 215-994-2488
TELEPHONE: 215-994-2222
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09621855
Patent No. 6346608
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lisa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fosberry, Andrew
Hodgson, John E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MecB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
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Best Local Similarity 22.6%
Matches 49; Conservative
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Shilling,
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                     121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVRQFANVV----NHIGGL 172
                                                                                                                                          463 K----PYSVILFDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIIMTSNVGAQ 517
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                                                                                                                                                                                                                             173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows 95
SOFTWARE: FRSEESD for Windows Version 2.0b
CURRENT WARPLICATION DATA:
APPLICATION NUMBER: US/09/040,843
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7.4%; Score 78.5; DE
Best Local Similarity 22.6%; Pred. No. 7;
Matches 49; Conservative 37; Mismatches
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FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jaworski, Deborah J.
Wang, Min
Shilling, Lisa K.
Burnham, Martin
Fosberry, Andrew
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Patent No. 6124119
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TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Dechert, Price & 4000 Bell Atlantic
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Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 866 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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US-08-219-262B-7
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ITILE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33.42
SEQ ID NO 19045
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
ACTION:
APPLICANT:
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1090-01-29
RIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7682
LENGTH: 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 MRNIEARGLKQMKRQGDANVKG-----EEGIVKAHLLIGVHD---DIVSMEYDL----A 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 YKLGDLHPTT-HVISDI------QDFVVALSL------EISDEGNITMTSFE 158
549 VGKTELARALAESMFGDDDAMIRVDMSEFMEKHAVSRLVGAPPGYVGHDDGGQLTEKVRR 608
                                               121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITMTSFEVROFANVV----NHIGGL 172
                                                                          609 K----PYSVILPDEIEKAHPDVFNILLQVLDDGHLTDTKGRTVDFRNTIIMTSNVGAQ 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 DPIHGTIRLTTLEIASINHPLFQRLRNIKQNSFLYKVFPSAVHSRFEHSLGVLHLSSEI- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 DPIHYD-KIT----EEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.3%; Score 78; DB 4; Length 511; Best Local Similarity 21.2%; Pred. No. 3.6; Matches 45; Conservative 38; Mismatches 75; Indels
                                                                                                                                         173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
                                                                                                                                                                                     664 ELQDORFAGFGGSSDGQDYETIRKTMLKELKNSFRPE 700
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                                                                                                                                                                                                                                                                                                Sequence 7682, Application US/09489039A
Patent No. 6610836
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7682
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APPLICANT: Marc J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 EYDLA--YKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMISFEVROFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----AADTG-----LQRAEAVAHAPGV 254
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: NAKHARIA, VIKRAM
APPLICANT: STEPHANIE A
APPLICANT: STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHARRACI EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            13 VAVSADPIHYDKITE--BINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIV-DFKG
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Query Match 7.3%; Score 78; DB 4; Length 516; Best Local Similarity 25.1%; Pred. No. 3.6; Matches 49; Conservative 27; Mismatches 55; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B

FILING DATE: 29-MAR.1994
ICLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 2,747-047-27
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Infectious bursal disease virus $2/70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 RLDQAAHHRVGD-----
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Best Local Similarity
Matches 39; Conserva
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us-10-024-955-7.rai

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(703) 413-3000
(703) 413-2220
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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Best Local Similarity
Matches 39; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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; STRAIN: 52/70
US-09-031-655-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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                                                                                                                                                                                                   US-09-031-655-7
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                                                                                                                                                                   RESULT 55
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                                                                                                                                                                                 157 ---NVINGEGVIVLSLPTSYDLGYVRLGDPIPAIGL----DPKWVATCDSSDRPRVYII 208
                                       99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VARBAM
APPLICANT: WATCHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON SPITTLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI 98
                                                                                                                                                                                                                                                                    155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                                                                                                                                                                                                                                                                                         7.3%; Score 78; DB 1; Length 1012; 23.2%; Pred. No. 10; ve 37; Mismatches 64; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REPERENCE/DOCKET NUMBER: 2747-047-27
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-320
TELEPHONE: (703) 413-320
TELEPHONE: (703) 413-320
TELEPHONE: (703) 413-320
TELERX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENMCTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Infectious bursal disease virus STRAIN: STC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08219262B
Patent No. 5788970
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1012 amino acids IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.2.
Best 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 54
US-08-219-262B-8
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Sequence 7, Application US/09031655

Sequence 7, Application US/09031655

Settle No. 601759

GENERAL INFORMATION:
APPLICANT: VAREARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
APPLICANT: MENGEL WHERSAT, STEPHANIE A
APPLICANT: MENGEL WHERSAT, STEPHANIE A
APPLICANT: MENGEL WHERSAT, STEPHANIE A
APPLICANT: SNYDER SELONA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
ADDRESSER: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1155 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::||:::||:::|
102 VSRSITVRSSTLPGGVYALNGTINAVTFQGSLSELTDVSYNGL----MSATANINDKIG- 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28; Gaps
155 TSPEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                              209 TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSVGGELVFQTSVQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 TAADDYQFSSQYQP-GGVTI--TLFSANIDAITSLSIGGELVFQTSVQ 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Score 78; DB 3; Length 1012; illarity 23.2%; Pred. No. 10; Conservative 37; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infectious bursal disease virus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOM, NOWNAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
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Sequence 31003, Application US/09252991A
Patent No. 6551795
BATENT NIN-6551795
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICANT NINGELINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 -----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTSFEVRQFANVVNHI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 QPNKEHMDMPSLHSLEHLTAELIRNHADYIV----DWSPMG--COTGF----YLTVLNHE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 GELAMR-NIEARGLKQMKRQGDANVKGEEGIVKAHLL-----IGVHDDIVSMEYDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
CORPATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
APPLICATION NOMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/085571
FILING DATE: JULY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...166
SEQUENCE DESCRIPTION: SEQ ID NO: 5004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGHE SOURCE:
ORGANISM: Enterococus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 GGLSILDPIFGVLSDVLTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 SYEDÍLDVLEATMKÖVLEA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5004:
                                                                                                                                                  NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 25.9
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-31003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
                                                                                             Sequence 8, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
APPLICANT: NYGHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MICKEL-WHERSAY, STEPHANIE A
APPLICANT: MICKEL-WHERSAY, STEPHANIE A
APPLICANT: MICKEL-WHERSAY, STEPHANIE A
ATITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TSFEVROFANVANHIGGLSILDPIFGVLSDVLTA-----IFQDTVR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: : ||: ||: ||: || : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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23.2%; Pred. No. 10;
iive 37; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Infectious bursal disease virus
STC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PCLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/219,262
FILING DATE: 29 + MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPHONE: (703) 413-320
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 57
US-09-107-532A-5004
; Sequence 5004, Application US/09107532A
; Patent No. 6583275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
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US-09-031-655-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                 361 DLFQLQKHRLQIAKRYIEKIQPSGGTNI--NEALLRAIFILNEANNLGLLDPNSVSLIIL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DPI- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 N-QDTSSQLKKEYNQVSTPLLRNVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGKFDPAK 537
                                                                                                                                                                                                                                                                                                                                  76 -----IEARGLKOWKRQGDANVKGEEGIVKAHLLIGVHDDIVSME---YDLAYK 121
                                                                                                                                                                                                                                     19 PIHYDKITEEINKAID--DAIAAIEQSETIDPWKVPDHADKFERHVGIVDFKGEL-AMRN 75
                                                                                                                                                                                          84; Indels 101; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     122 LGDLHPTT------HVISDIQDFVVALSL-------EISDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 FGVLSDVLTAI--------FQDTVRKEMTKVLAPAFKREL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Batterson, Chandra
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
TITLE OF INVENTION: INHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                      Query Match
7.3%; Score 77.5; DB
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 6.1/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 NITMISFEVROFANVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect 6.1/MS-DOS 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/388,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,579
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0505 US
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NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09388774 Patent No. 6228991 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 946 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                    IMMEDIATE SOURCE:
LIBRARY: GENEBANK
CLONE: gi33985
US-09-074-579-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-09-388-774-3
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                                                                                                                                                                                                                                                                                                                                                                                                                     23 DKITEBINKAIDDAIAAIBQSETIDPMKVPDHADKFER------HV-GIVD-----F 67
                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                   Query Match 7.3%; Score 77.5; DB 4; Length 409; Best Local Similarity 24.2%; Pred. No. 2.9; Matches 40; Conservative 28; Mismatches 62; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 L------HPTTHVISDIQDFVVALSLEISDEGNITMTSFEVR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09074579;
Patent No. 6001596;
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Patterson, Chandra
ITILE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
ITILE OF INVENTION: IMHIBITOR HEAVY CHAIN PRECURSOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTINUED READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMBUTER: IBM Compatible

COMBUTER: IBM Compatible

COMBUTER: Word Perfect 6.1/MS-DOS 6.2

SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,579

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION NUMBER:

FILING DATE:

ATRONEY/ACENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REGISTRATION NUMBER: 39,132

REGISTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
; CURRENT APPLICATION NUMBER: US/09/252,991A; CURRENT FILING DATE: 1999-02-18; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR FILING DATE: 1998-02-18; PRIOR APPLICATION NUMBER: US 60/094,190; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 31003; LENGTH: 409
                                                                                                                                                                                                                                                , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 946 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
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STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-074-579-3
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GENERAL INFOCRATION:
CERREAL INFOCRATION:
TITLE OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy
PILE REPERENCE: FSU-99XCI
CURRENT APPLICATION NUMBER: US/09/425,453A
CURRENT FILING DATE: 1999-10-22
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 20
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 1480
                                                                  APPLICANT: Teem, John L.
TILLS OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy
TILLS OF INVENTION: CFTR Genes and Proteins for Cystic Fibrosis Gene Therapy
CURRENT APPLICATION NUMBER: US/09/425,453A
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,444
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 GIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 FEVRQ--FANVANHIGGLSILDPIFGVLSDVLT--AIFQDTVRKEM---TKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               551 GQMARISLARAVYKDADLYLLDSPFGYL-DVLTEKEIFESCVCKLMANKTRILVTSKMEH 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 GIVKAHILIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 FEVRO--FANVVNHIGGLSILDPIFGVLSDVLT--AIFODTVRKEM---TKVLAPAFKRE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 GTIKENIIFGV-----SYD-EYRYRSVIKACQLEEDISKFAEKDNM-VLGEGGITLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%; Score 77.5; DB 4; Length 1480; Best Local Similarity 28.5%; Pred. No. 21; Matches 35; Conservative 21; Mismatches 50; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
7.3%; Score 77.5; Di
Best Local Similarity 28.5%; Pred. No. 21;
Matches 35; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 63
US-09-425-453A-18
; Sequence 18, Application US/09425453A
; Patent No. 6468793
; GENERAL INFORMATION:
         Sequence 8, Application US/09425453A
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-425-453A-18
                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(1480)
US-09-425-453A-8
                               Patent No. 6468793
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 LEK 212
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                                                                                                                                                                                                                                                                                                      LENGTH: 1480
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Patent No. 6562958
GENERAL INFORMATION:
PAPLICANT: GATY L. Barton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PB
CURRENT FILING DATE: 1999-06-04
NUMBERT OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                            -----IEARGLKOMKRQGDANVKGEEGIVKAHLLIGVHDDIVSME---YDLAYK 121
                                                                                                                                                                                                                                                                                                                                                                      | | ::::: | | ::| | 361 DLFQLQKHRLQIAKRYIEKIQPSGGTNI--NEALLRAIFILNEANNLGLLDPNSVSLIIL 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----DPI- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSME--YDLAYKLGDLHPTTH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153 FRNISFDELK------ENYIEATHALIEGGADIILIETVFDTLNCKAAIFAVKE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 VISDI-QDFVVALSLEISDEGNITMISFEVRQFANVVNH----IG----GLSILDPIF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 VFKQIGRELPIMISGTITDASGRTLTGQTAEAFWNSVRHGDLLSIGFNCALGADAMRPHV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 N-QDISSQLKKFYNQVSTPLLRNVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGKFDPAK 537
                                                                                                                                                                                                                                                   19 PIHYDKITEEINKAID--DAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL-AMRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 VSADPIHYDKITEEINK-AIDDAIAAIEQSETID-PMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                      84; Indels 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FODIVRKEMIKVLAPAFKREL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 LDQIESVITATSANTQLVLETLAQMDDLQDFLSKD--KHADPDFTRKL 583
                                                                                                                                                                Length 946;
                                                                                                                                                             DB 3;
                                                                                                                                                         Query Match
7.3%; Score 77.5; Di
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  122 LGDLHPTT------HVISDIQDFVVALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Acinetobacter baumannii
US-09-328-352-5704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 NITMTSFEVRQFANVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 FGVLSDVLTAI-----
STRANDEDNESS: single;
TOPOLOGY: linear;
IMMEDIATE SOURCE:
LIERRAY: GENEBANK;
CLONE: gi33985
US-09-388-774-3
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Best Local Similarity
Matches 50; Conserval
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US-09-328-352-5704
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SEQ ID NO 5704
THNGTH: 1233
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US-09-425-453A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL----DPXMVATCDSSDRPRVYTI 208
                                                                              APPLICANT: VARHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MEMBEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 ISFEVRQFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.2%; Score 77; DB 1; Length 1012; Best Local Similarity 23.4%; Pred. No. 13; Matches 39; Conservative 36; Mismatches 64; Indels 3
                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOCR CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F 4,618
REGISTRATION NUMBER: 2747-047-27
TELEFROMONICATION INFORMATION:
TELEFROMONICATION INFORMATION:
TELEFRAX: (703) 413-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Infectious bursal disease virus
STRAIN: E/DEL
US-08-219-262B-3
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              Sequence 3, Application US/08219262B Patent No. 5788970 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1012 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                              USA
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US-08-219-262B-5
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-08-219-262B-3
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Sequence 5, Application US/08219262B Patent No. 5788970 GENERAL INFORMATION: APPLICANT: VAKHARIA, VIKRAM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENGEL-WHERSAT, STEPHANIE A
FENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
VENTION: CHAR CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
FENTION: THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
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                             TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE V.
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIEGHINIA
COUNTRY: USA
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STREET: 655 Fifteenth Street, N. W.,
STREET: Suite 330 - G Street Lobby
                                                                                                                                                                                                                                                                            COMPUTER RELABBLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REPERENCE/POCKET NUMBER: 2747-047-27
TELECOMMUNICATION INDEMARIED:
TELECOMMUNICATION INDEMARIED:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Infectious bursal disease virus CU-1
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TELEFAX: (703) 413-220
TELEX: 24885 OPAT UNIFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-219-262B-5
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Best Local Similarity 23.4
Matches 39; Conservative
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
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STRAIN: E/DEL
                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENCEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%; Score 77; DB 2; Length 1012; 23.4%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Indels
                               COUNTRY: USA
ZIP: 2005-5701
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/708,541A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONIGE C.
REGISTRATION NUMBER: 36.105
REFERENCE/DOCKET NUMBER: P8172-6002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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MEDTUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09031655
Patent No. 6017759
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IXPE: amino acid
TOPOLOGY: linear
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-708-541A-30
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THICK ATPUTIONE NAME AND 60/219,262

TTICKED DATE: NAME AND 61/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/2004 (1) 10/200
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TELECOMMUNICATION INFORMATION:
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US-09-107-532A-3785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKRQGDANVKGEEGI
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Patent No. 6596280
GENERAL INFORMATION:
APPLICANT: WAKHARIA, Vikram N.
APPLICANT: MUNDT, Egbert
TITLE OF INVENTION: A METHOD FOR GENERATING BIRNAVIRUS
TITLE OF INVENTION: FROM SYNTHETIC RNA TRANSCRIPTS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20036-5339
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/147,771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 31-JUL-97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/708,541
FILING DATE: 05-SEP-96
ATTORNEY/AGENT INFORMATION:
NAME: KTTS, MOBILE 36,105
REFERENCE/DOCKET NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P108288-09002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/198,913
FILING DATE: 24-NOV-98
APPLICATION NUMBER: PCT/US97/12955
    REGISTRATION NUMBER: 24,618
REFERENCS/DOCKET NUMBER: 2747-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 23.49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
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US-09-147-771-30
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Matches
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Sequence 3785, Application US/09107532A
Sequence 3785, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                 99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
                                                                                                                                                                                                                                                                                                                                     40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                             28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 ISPEVROFANVVNHIGGLSILDPIFGVLSDVLTA-----IFQDTV 194
                                                                                                                                                                                                                                          7.2%; Score 77; DB 4; Length 1012; 23.4%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
COMPUTER: PC
COMPAGE: ACIA
SOFTWARE: ACIA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,71
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.4%; Pred. No. 13;
Matches 39; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 429 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3785:
SEQUENCE CHARACTERISTICS:
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 1012 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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-09-252-991A-22095
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                    RLSRDQAITVLQEEEITAEKSQVSPYGIVAKKGHLASSSLFHD--GVM-----TI 255
                                                                                                                                                                                                           91 KKVDDWVKTLLYLSVYQLEFLD--KVPAHAILNEA-VEIAKVKGNPGTGKFVNGVLRNYQ 147
                                                                                                                                                                                                                                                  RQGDANVKG-----EEGIVKAHLLIGVHDDIV-SMEYDLAYKLG-DLHPTTHVIS--DIQ 136
                                                                                                                                                                                                                                                                          137 DFVVALSLEISDEGNITMISFEVROFANVV--NHIGGLSILDPIFGVLSDVLTAIFQDTV 194
                                                                                                                                                                        31 KAIDDAI----AAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMK 85
                                                                                                                                      Gaps
                                                                                                                                      31;
                                                                                             7.2%; Score 76.5; DB 4; Length 429;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/05,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                         Best Local Similarity 24.4%; Pred. No. 4.1,
Matches 48; Conservative 34; Mismatches
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...429
SEQUENCE DESCRIPTION: SEQ ID NO: 3785:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 164 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6514:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                               CDESSMLVAPSMQIEPE 272
                                                                                                                                                                                                                                                                                                                                                                                                      195 RKEMTKVLAPAFKRELE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-107-532A-6514
                                                        US-09-107-532A-3785
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                                                                                                                                                                                                                                                                                                                                                                                                                                             256
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                                                                                           Query Match
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 10196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Sequence 3947, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                              -----SFEVROFANV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 KGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLH-PTTHVISDIQDFV-VALSLEISDEG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 VMEYKFNLNLKEV-----LPTQGTININGQDNDDDIVIKK---IEFIDSDINVFFYSK
                                                                                                                                                                                                                                                                                                                                                                                                                            58 EKLADFSNIAEMIERLKDFMISVWDVAMLADESNYTSSIYRLEDSNWIEISLELKTLPNS
                                                                                                                                                                                                                                                                       64 IVDFKGELAMRNIEARGLKQMKRQGDANVKGEEG----IVKAHLLIGVHDDIVSMEYDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GELAMRNIEARGLKOMKROGDANV
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       28;
                                                                                                                                                          7.1%; Score 76; DB 4; Length 164; 20.2%; Pred. No. 1.1; ive 30; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 76; DB 4; Length 645; 24.0%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                           120 YKLGDLHPTTHVISDIQDFVVAL--SLEISDEGNITMT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : ||: | |: | | : 1 | : 1 | 147 FLDVAG-TAHAFGGFVDHRRG-TLADPVLAHRGD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 NITMISFEVROFANVVNHIGGLSILDPIFGVLSD 184
NAME/KEY: misc_feature;
LOCATION: (B) LOCATION 1...164;
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US-09-107-532A-6514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 IDPMKVPD-HADKFERHVGIVDFK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22095, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEI
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
                                                                                                                                                    Query Match
Best Local Similarity 20.2%
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37; Conservative
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Matches 37; Conserv
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Sequence 5426, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICAMY: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5426
LENGTH: 441
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US-09-134-000C-4810
Sequence 4810, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
PAPLICANT: LYND NOUCLE-Stamm et al
PITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 YKLGDLHPT-THVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSIL--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 VGIVDFKGELAMRNIEARGLKQM--KRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 AGAG---PTASAVVADVIDIVRDISYTEDGAGTIPQLAFEA-----LTNMPILSRE 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 DQHVAAVAURLVENRRQFLQGVVAVAVIAIAIGGFEHHHVGPAQRRGRAHQRRAGVAEVA 243
                                                                                                                                                                                                                                                                                                                                                                   128 LAVAVVELVAVA----QVDAIGTGGHRAVEEYRLLRQAALLVEAAEVVEQVLGAADGERR 183
                                                                                                                                                                                                                                                                                                                      5 LLIAAVAFVAVSADPIHYDKITEEINKAIDD-----AIAAIEQSETIDPMKVPDHADKF 58
                                                                                                                                                                                                                                                                                                                                                                                                                       ----EARGLKOMKROGDANVK 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KFLLIAAVAFVAVSADPIHYDKI-TEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AIFQDTVRKEMTKVL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                355 EMTTGYYIRLNAEDQTGVLADVTTILSRAGISIDAIMQQSRLKDLIPIV 403
                                                                                                                                                                                                                          Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 441;
                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                       7.1%; Score 75.5; DE 21.2%; Pred. No. 5.2; tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 75.5; DE 23.1%; Pred. No. 5.5; ative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          ----FKGELAMRNI---
MBER: US 60/094,190
1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Acinetobacter baumannii
US-09-328-352-5426
                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 GKHQAARLHLVVELHFD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 GEEGIVKAHLLIGVHDD 110
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Best Local Similarity 23.1%
Matches 53; Conservative
                                                                                                                                                                                                                                                                         Conservative
  PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1998-0
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 21128
LENGTH: 423
                                                                                                                                                                                                                                                                                                                                                                                                                            ERHVGIVD----
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                             US-09-252-991A-21128
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US-09-328-352-5426
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US/00/4,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 MRNIBARGLKQMKRQGDANVKGBEGIVKAHLLIGVHDDIVSMEYDLAYKLG--DLHPTTH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 VISDIQDFVVALSLEISDEGNITMTSFEVRQFANV-VNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            916 ERNREQKA--RLSEQSKLEVQKD----RAEMILDNHLTYLQSEYQLTFEKASQDYQETTD 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 VSADPIHYDKITEEINKAIDDAIAAIEQSETI--DPMKVPDHADKFERHVGIVDFKGELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 76; DB 4; Length 1196; Best Local Similarity 22.2%; Pred. No. 22; Matches 45; Conservative 41; Mismatches 93; Indels 3
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

// LCCATION: (B) LOCATION 1...1196

SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

US-09-107-532A-3944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027 DEMDDEVRTRFKEVFEAIRQEFK 1049
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- FQDTVR---KEMTKVLAPAFK 207
                                                                                                                                                   COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1196 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3944:
SEQUENCE CHARACTERISTICS:
                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 74
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APPLICANT: VAKTARIA, VIKRAM
TITLE OF INVENTION: NOVEL INFECTIOUS BURSAL DISEASE VIRUS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Indels
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1755 S. Jefferson Davis Highway, Suite 400
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209 TAADDYQFSSQYQS-GGVTI--TLFSANIDAITSL 240
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REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2284-029-0 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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APPLICATION NUMBER: US/07/944,943
FILING DATE: 19920915
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                  546 MAGDAGRGFAVVADEVQRLA 565
                                                                                                                                                          154 MISFEVRQFANVVNHIGGLS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/07944943
Patent No. 5518724
GENERAL INFORMATION:
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; Sequence 2. Application US/07944525
; Patent No. 5632989
; GENERAL INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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TELEFAN 24865 OPAT UR
TELEX 24865 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 36; Conserva
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STATE: Virginia
COUNTRY: U.S.A.
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STREET: 17
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S-05-25-991A-16965
S-05-25-991A-16965
S-05-25-991A-16965
S-05-25-991A-16965
GENERAL INFORMATION:
MAC J. Rubenfield et al.
TITLE OF INVENTION:
MAC J. REPEREBERTE
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/094,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 YFATYVFEKGADIPALLGAYILEGSKAGATAASVWAAHHVLPLNVAGYGKLIGAS-IEGS 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 HDDIVSMEYDLAYKLGD----LHPTTHVISDIQDFVV------ALSLEISD--- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | | : | | : | | HFYNFLNDLTFKVGDKEIEVHTLTFPFNRWDYVFKEKGNDDLVAMNKLNHDVYDYAS 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 EEINKAIDDAIAAIE--QSETIDPMKVPDHADKFERHVGIVDFK-GELAMRNIEARG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 75.5; DB 4; Length 608; Best Local Similarity 21.0%; Pred. No. 9; Matches 56; Conservative 37; Mismatches 71; Indels 103
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FILE REFERENCE: 032796-032;
CURRENT APPLICATION NUMBER: US/09/134,000C;
CURRENT FILING DATE: 1998-08-13;
FRIOR APPLICATION NUMBER: US 60/055,778;
FRIOR FILING DATE: 1997-08-15;
NUMBER OF SEQ ID NOS: 6812;
SOFTWARE: Patentin version 3.1;
SOFTWARE: Potentin version 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 MTPYMND---KEEFDVYAPKIQAALQE 599
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16965
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-09-134-000C-4810
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SP
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid STRANDEDNESS: unl
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US-08-219-262B-2
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APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHEREAT, STEPHANIE A
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THERBON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: LUETTICKEN, HEINRICH D.
TITLE OF INVENTION: ATTENUATED, LIVE VACCINE FOR DELAWARE
TITLE OF INVENTION: STRAIN IBDV
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                        COUNTRY: C.C...

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/944,525
FILING DATE: 19920914
CLASSIFTATION NUMBER: 235
ATORNEY/AGENT INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 2284-028-0 CIP
TELECOMMUNICATION NUMBER: 22003
TELECOMMUNICATION NUMBER: 10003
TELECOMMUNICATION 143-2000
                                                                                                        ADDRESSEE: OBLON, SPLVAK, MCCLELLAND, MALER AND ADDRESSEE: NEUGRADT, P.C. STREET: 1755 JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR CITY: ARLINGTON
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Patent No. 5788970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 1012 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703) 413-300
TELEPAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.1%
Best Local Similarity 23.2%
Matches 36, Conservative
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US-08-219-262B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKRQGDANVKGEEGI
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLESSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 247-047-27
TELEFOND: (703) 413-3000
TELEFAX: (703) 413-320
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
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TELEFAX: (103) 413-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Infectious bursal disease virus
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5788970
GENERAL INFORMATION:
APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHA
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(703) 413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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; STRAIN: D78
US-08-219-262B-4
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  TELEFAX:
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APPLICANT: VAKTARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHIMERIC INFECTIONS EVENESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEB: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
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CONTINE CALOUS
COMPUTER FELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219, 262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24, 618
REFERENCE/DOCKET NUMBER: 27,77-047-27
TELECOMMUNICATION INFORMATION:
TELEFHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAI 189
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                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Infectious bursal disease virus STRAIN: DS326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 4, Application US/08219262B
; Patent No. 5788970
                  CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3200
TELEFAX: (703) 413-3200
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 anino acids
TYPE: amino acid
STRANDEDNESS:
FILING DATE: 29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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US-08-219-262B-4
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Sequence 12. Application US/08219262B

Batent NO. 5788970

GENERAL INFORMATION:
APPLICANT: VAREARIA, VIKRAM
APPLICANT: MANGEL-WHERSAT, STEPHANIE A

TITLE OF INVENTION: CHITERIC INFECTIOUS BURSAL DISEASE VIRUS

TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 VSRSLTVRSSTLPGGVYALNGTINAVTFQGSLSELTDVSYNGL----MSATANINDKIG- 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.1%; Score 75.5; DB 1; Length 10 Best Local Similarity, 23.2%; Pred. No. 20; Matches 36; Conservative 35; Mismatches 63; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
COMPUTER: ENDABLE FORM:
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,262B
FILING DATE: 29-MAR-1994
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: COBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEBPAX: (703) 413-2200
TELEBPAX: (701) 413-2200
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                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Infectious bursal disease virus
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TELEX: 248855 OPAT UR
INFORMATION FOR EQO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino aci
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99 VKAHLLIGVHDDIVSM--EYDLAY-KLGDLHPTTHVISDIQDFVVALSLEISDEGNI-TM 154
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157 ---NVLVGEGVTVLSLPTSYDLGYVRLGDPIPAIGL-----DPKMVATCDSSDRPRVYTI 208
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VARHARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: SNYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 IEOSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKROGDANVKGEEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STRET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR CITY: ARLINGTON STATE: VIRGINIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                      155 TSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                                                            209 TAADNYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
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23.2%; Pred. No. 20;
:ive 35; Mismatches
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: 0BLON NORMAN F
REGISTRATION NUMBER: 2747-047-27
TELEPHONE: (703) 413-3000
TELEPHONE: (703) 413-2200
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09031655
Patent No. 6017759
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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STRANDEDNESS: unl
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
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                                                                                                                                                                                                                                                                       US-09-031-655-1
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Patent No. 5788970
GENERAL INFORMATION:
APPLICANT: VARGARIA, VIKRAM
APPLICANT: SNYDER, DAVID B
APPLICANT: MINGEL WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: THERBON
TITLE OF INVENTION: THERBON
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                                                                                                                                                                                                        40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKQMKRQGDANVKGEEGI
                                                                         DB 1; Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSFEVROFANVVNHIGGLSILDPIFGVLSDVLTAI 189
                                                                      7.1%; Score 75.5; DE 23.2%; Pred. No. 20; ive 35; Mismatches
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; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 274
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONB: (703) 413-2300
TELEPAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
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Best Local Similarity 23.29
Matches 36; Conservative
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TOPOLOGY: linear
TECHLE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                  Best Local Similarity
Matches 36; Conserv
       JS-08-219-262B-12
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                                                                             Query Match
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Patent No. 6017759
GENERAL INFORMATION:
APPLICANT: VAKHAR
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                                                                                                                                                                                 Sequence 2, Application US/09031655;
Patent No. 6017759
GENBRAL INFORMATION:
APPLICANT: VAKHARIAN, VIKRAM
APPLICANT: WINDER, DAVID B
TITLE OF INVENTION: CHIMERCAT, STEPHANIE A
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: 15
CORRESPONDENCE ADDRESS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUNTRY: UXSAILER
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
FILING DATE: 2 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
MARE: OBLOW, NORMAN F
REGISTRATION NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
MATCHER COMMUNICATION INFORMATION INFORM
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STRAIN: DS326
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TELEPAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 23.2%
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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USA
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US-09-031-655-2
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US-09-031-655-4 Sequence 4, Application US/09031655

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APPLICANT: VACTARIA, VIKRAM
APPLICANT: VACTARIA, VIKRAM
APPLICANT: SUNDER, DAVID B
APPLICANT: SUNDER, DAVID B
APPLICANT: MENGEL-MERRAT, STEPHANIE A
ITILE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
ITILE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
ITILE OF INVENTION: THEREON
CONRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ALLINGTON
STARE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTED ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 TSFEVROFANVNHIGGLSILDPIFGVLSDVLTAI 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATE:

APPLICATION NUMBER: US/09/031,655
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F, REGISTRATION NUMBER: 2747-047-27
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 41-320
TELECATION OF 850 ID NO: 4:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 4:
LENGTH 1112 anino acids
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SNYDER, DAVID B
MENGEL-WHERSAT, STEPHANIE A
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Sequence 12, Application US/09031655

Pattent No. 6017759

GENERAL INFORMATION:

APPLICANT: VAKHARIA, VIKRAM

APPLICANT: NAKHARIA, VIKRAM

APPLICANT: MENGEL-WHERSAT, STEPH

APPLICANT: MENGEL-WHERSAT, STEPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 23.24
Matches 36; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON NORMAN F
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2747-047-27
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
TELECHONUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1012 amino acids
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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US-09-252-991A-24505
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CRGANISM: Pseudor
US-09-252-991A-24505
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    COUNTRY:
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APPLICANT: VAKHARIA, VIKRAM
APPLICANT: SAYDER, DAVID B
APPLICANT: MENGEL-WHERSAT, STEPHANIE A
TITLE OF INVENTION: CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS
TITLE OF INVENTION: CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED
TITLE OF INVENTION: THEREON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SEPVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEPPERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGON
CHIMERIC INFECTIOUS BURSAL DISEASE VIRUS CDNA CLONES, EXPRESSION PRODUCTS AND VACCINES BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 IEQSETIDPMKVPDHADKFERHVGIVDFKGELA-MRNIEARGLKOMKRQGDANVKGEEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 1012;
                                                                                                              ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVID HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.1%; Score 75.5; DE 23.2%; Pred. No. 20; tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US 08/219,262
FILING DATE: 29-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN FREISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
FILING DATE:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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703) 413-2220
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Best Local Similarity 23.2*
Matches 36; Conservative
TITLE OF INVENTION: CHIM
TITLE OF INVENTION: CBNA
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-031-655-12
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                    VIRGINIA
                                                                                                                                                                                                          COUNTRY: USA
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Sequence 24505, Application US/0925291A
Sequence 24505, Application US/0925291A
Sequence 24505, Application US/0925291A
Sequence 24505, Application US/0925291A
Sequence 24505, Application US/0925291A
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE
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: : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : | |: : : : | |: : : : : | |: : : : : | |: : : : : | |: : : : | |: : : : : | |: : : : : | |: : : : | |: : : : | |: : : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : : | |: : : : | |: : : : | |: : : : | |: : : : : | |: : : : | |: : : : : | |: : : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | | |: : : : | |: : : : | |: : : : | |: : : : | |: : : : | |: : : | |: : : : | |: : : : | |: : : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : : | |: : 
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7.0%; Score 75; DB 4; Length 193; Best Local Similarity 21.7%; Pred. No. 1.8; Matches 39; Conservative 33; Mismatches 84; Indels
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STATEM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 TAADNYQFSSQY-QTGGVTI--TLFSANIDAITSL 240
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREKGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A
CURRENT PFLING DATE: 1999-02-18
PRIOR PLILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
                                                                     13;
                                                                                                                                                                                                           62 VGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYK 121
                                                                                                                                                                                                                                                                                                       122 LGDLHPTTHVISDIQDFVVALSL-EISDEGNITMTSFEVRQFANVVN-HIGGLSILDP-- 177
                                                                                                                                                                                                                                                                                                                                                 180 AGEL-------AAVDLGALGDLGNLAF--HPGRQFGNAFQLPTGQLDLADPFP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 GVGLLDOQVVLEIEGIEBERHP--VDARABLGDFQLEFLDIAEVVRLFALDPLOFLQRRAQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ARGLKQMKRQG------DANVKGEEGIVKAHLLIGVHDDIVSMEY 116
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                                                                                                                                                  146 LGLV---LQLAGSFAEAQGL-----FLAGAE--VAAHLL-----DRGEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 LGPAAAGQRDAPRMGRAQGADDVDARRVAVVADAGADGLEGVGAGDVALDQVGQLQVLEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 -VOHRFVDIAPGNADLLAVLHVGNGTPADGLLDGLLDVFTVAPQEALAVHRALVLA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0%; Score 75; DB 4; Length 508;
18.3%; Pred. No. 7.8;
ive 38; Mismatches 105; Indels
                   7.0%; Score 75; DB 4; Length 482;
28.4%; Pred. No. 7.2;
tive 21; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 ---TIDPMKVPDHADKFERHVGIVDFKGELAMRNIE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-252-991A-17386
; Sequence 17386, Application US/09252991A
; Patent No. 6551795
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Patent No. 6583275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17386
LENGTH: 508
                                                                     Conservative
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224 QLFGKLADLL 233
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                                            Similarity
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nes 54; Conserv
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                                                                     54;
                   Query Match
Best Local S:
Matches 54,
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Best Local S:
Matches 54
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                                                                                                                                                                                                                                                                                                                                  Sequence 3313. Application US/09540236

Sequence 3313. Application US/09540236

Batent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACLD AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

SEQ ID NO 3313

LENGTH: 458
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUPTIONS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUPTIONS OF SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUPTION SECURES: 105/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23313
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                                                                                                                                                                                                              | ::|| | ; ; ; ; | | 1 ; ; ; | 1 ; ; ; | 1.89 | 182 TKLKTÇMLSDEN--VPSSRIKVVTENGIVYMMGLVNQQEAAQAVRVAQGVDGVQKIVKLF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAYKLGDLHPTTHVISDIQDFVVALSL-------EISDEGNI---TMTS-FEV 159
                                                                                      ELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDI-VSMEYDLAYKLGDLHPT 128
                                                                                                                              80 IVLIAGQIPR-----ADLKSKAEQAARIVQKVKNVHNELQVISPSSLLARNNDAWIT 131
                                                                                                                                                                                  ----THVISDIQDFVVALSLEISDEGNIT-----MTSFEVRQFANVVNHIGGLSILDPIF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 LRVHPTLIPSQALL------AVANAVMIDAHPLGQSLDYG 321
                        23 SFLSATRDKPIDDDRGTRTIGSKIDDSL--IETKAAVNIAKADPALDK-DSHIVVVSYNG 79
AFVAVSAD-PIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KFLLIAAVAFVAVSADPIHYDKI-TEEINK-AIDDAIAAIEOSETIDPMKVP---DHADK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 RQFANVVNHIGGLSILDPIFGVLSDVLTAIFQD 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R------LIVKDE-GGVLADT-TRILSD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 75; DB 24.4%; Pred. No. 6.7; iive 30; Mismatches
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 24.4'
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: M.catarrhalis
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                                                                                                                                                                                                                                                                                                  RESULT 91
US-09-540-236-3313
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Sim & McBurney
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amino acid
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                                                                                                                                                                                   ADDRESSEE: Sim & STREET: 6TH Floor CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7
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               APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS PAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LREADCSIAMAEGDGATRQIAN-----LVLLDSDFTTLPEVLFEGRRVVNNVTKVSGI 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 FERHVGIVDFKGELAMRNIEAR----GLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 SMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 YDAYYDLSQITEEMEVREAAHRYTVFGRVSPQQKKLLVNELKESGRTVAMTGDGVNDVLA 492
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                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 AFVAVSADPIHYDKITEEINKAIDDAIAAIEOSETID----
                                                                                                                                                                                                                                                                                        COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: ASCII
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...729
; SEQUENCE DESCRIPTION: SEQ ID NO: 6946:
US-09-107-532A-6946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 729 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 6946:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                       STATE: Massachusetts
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                NUMBER OF SEQUENCES:
GENERAL INFORMATION:
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Sequence 2, Application US/08433522A Patent No. 6013514 GENERAL INFORMATION:

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---EGIV-----KAHLLIGVHDDIVSMEY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 SLTFKGNESVSSSTLQEQMELQPDSWWKLWGNKFEGAQFEKDLQSIRDYYLNNGYAKAQI 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 797;
APPLICANT: CHONG, Pele
APPLICANT: THOYAS, WAYNE
APPLICANT: THOYAS, WAYNE
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, DWO YUAN Charles
APPLICANT: KIEIN, Michel
TITLE OF INVENTION: HARMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI----
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
GLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                              6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 19.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08433522A Patent No. 6013514 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTVRKEMTKVLAPAFKREL 210
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US-08-433-522A-4
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STREET: 6TH Floc
CITY: Toronto
STATE: Ontario
                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 75; DB 3; Length 797; Best Local Similarity 19.4%; Pred. No. 16; Matches 62; Conservative 49; Mismatches 88; Indels 3
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: LOCSMORE, Sheena
APPLICANT: LOCSMORE, Sheena
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCES: 55
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRILING DATA: 12-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acid
                                                                                                                                    Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTFRESDIADVENAIKAKL 309
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                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-4
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STREET: 611.
-mv: Toronto
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Sequence 6, Application US/08433522A; Patent No. 6013514; GENERAL INFORMATION:

US-08-433-522A-6

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----EGIV-----KAHLLIGVHDDIVSMEY 116
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APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 OVERMATION SISTEM: EV-DUSYMB-BUSS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,522A
FILING DATE: 12-SEP-1995
CLASSIFICATION: 435
ATTONENTY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REPRENCE/POCKET NUMBER: 24,973
REPRENCE/POCKET NUMBER: 1038-434 MIS:jb
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 aning acids
LENGTH: 797 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI-
                                                                                                                                                                                                 E: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 DIVRKEMIKVLAPAFKREL 210
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                                                                                                                                                                                                                                                                                          COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 797 amino acids
amino acid
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MOLECULE TYPE: protein
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7.0%; Score 75; DB 3; Length 797;
Best Local Similarity 19.4%; Pred. No. 16;
Matches 62; Conservative 49; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI-----
APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Bing
APPLICANT: YANG, Yan Shena
APPLICANT: LOCSMORE, Sheena
APPLICANT: KIEIN, Michel
APPLICANT: KIEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SUCHBUCES: 55
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                E: Sim & McBurney
6TH Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038-829 MIS:jb
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
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NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 599-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-135-166-2
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                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 DLAYKLG---
                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                        Ontario
                                                                                                                                                           STREET: 6TH FA
                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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----EGIV------KAHLLIGVHDDIVSMEY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 120; Gaps
APPLICANT: CHONG, Pele
APPLICANT: THOYAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Man.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 797;
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
7.0%; Score 75; DB 3
Best Local Similarity 19.4%; Pred. No. 16;
Matches 62; Conservative 49; Mismatches
                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038-829 MIS:jb
                                                                                                                                                                                                                                                                                   STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PARIOR APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 DIVRKEMIKVLAPAFKREL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWARY, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 KRQGDANVKGE------
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TOPOLOGY: limit
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291 DTFRRSDIADVENAIKAKL 309

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 MKFLLIAAVAF---VAVSADP----IHYDKITEEINKAI------DDAIAAI
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                                                                                              APPLICANT: THOMAS, Wayne
APPLICANT: YANG, Yan Ping
APPLICANT: YANG, Yan Ping
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
NUMBER OF SEQUENCES: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,166
                                                                                                                                                                                                                                                                                         3: Sim & McBurney
6TH Floor, 330 University Avenue
Sequence 6, Application US/09135166
Patent No. 6083743
GENERAL INFORMATION:
APPLICANT: THOWAS, Wayne
APPLICANT: THOWAS, Wayne
APPLICANT: LOOSMORE, Sheena
APPLICANT: SIA, Dwo Yuan Charles
APPLICANT: KLEIN, Michel
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 10;
TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS: LENGTH: 797 aming
                                                                                                                                                                                                                                                                                                       STREET: 6TH Floor, 330
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy di
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ADDRESSEE: Sim & MCE
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Db 237 TKTDVQLNDEKTKVNVTIDVNEGLQYDLRSARIIGNLGGMSAELEPLLSALH-----LN 290
QY 192 DTVRKEMTKVLAPAFKREL 210
Db 291 DTFRRSDIADVENAIKAKL 309
Search completed: August 6, 2004, 16:02:40
JOb time: 24 secs
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2 US-10-282-122A-54874
5 US-10-369-493-39287
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Sequence 7, Appli
                                                                                                                                                         2004, 16:01:47; Search time 45 Seconds (without alignments) 1484.766 Million cell updates/sec
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                       GenCore version 5.1.6
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Maximum Match 100%
Listing first 100 summaries
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length: 2000000000
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RESULT 3
US-09-847-208-85
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 Sequence 126, App
Sequence 68540, A
Sequence 73215, A
Sequence 75259, A
Sequence 76037, A
Sequence 10901, A
Sequence 13037, A
Sequence 118847,
Sequence 116, App
Sequence 126, App
Sequence 150, App
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Publication No. US20020168373A1
GENERAL INFORMATION:
APPLICANT: Wayne R. Thomas and Kaw-Yan Chua
TITLE OF INVENTION: Allergenic Proteins and Peptides From
                                                                                                                                                                                                                                                                                                   Sequence 77, Application US/09847208

Publication No. US20030082190A1

GENERAL INFORMATION:
APPLICANT: Shang, Ke
APPLICANT: Zhang, Ke
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
TITLE OF INVENTION: 1GE-MEDIATED ALLERGIC DISEASES
TITLE OF INVENTION: 1GE-MEDIATED ALLERGIC DISEASES
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER FILING DATE: 2001-05-01
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 77

LENTH: 213
5 US-10-093-463-126
2 US-10-282-122A-68540
2 US-10-282-122A-75215
2 US-10-282-122A-75259
2 US-10-282-122A-76037
2 US-10-282-122A-76037
2 US-10-282-122A-76037
0S-09-815-242-1001
US-10-282-122A-53037
6 US-10-282-122A-53037
5 US-10-2893-126
5 US-10-834-149
4 US-10-219-834-149
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US-09-847-208-77
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                ALIGNMENTS
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STATE: Massachusetts
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US-10-024-955-7
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100.0%; Score 1068; DB 13; Length 213;
Best Local Similarity 100.0%; Pred. No. 3.8e-102;
Matches 213; Conservative 0; Mismatches 0; Indels 0;
                                                            COMPUTER READABLE FORM
MEDIUM TYPE: FOLDPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/024,955
FILING DATE: 19-Dec-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1996
APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1996
APPLICATION NUMBER: US/08/553,336A
FILING DATE: 10-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REGISTRATION NUMBER: MI-032CP2
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ; ORGANISM: Dermatophagoides pteronyssinus (House-dust mite) US-09-847-208-85
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; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew; APPLICANT: Saxon, Andrew; APPLICANT: Zhang, Ke
; APPLICANT: Zhang, Ke
; TILLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TILLE OF INVENTION: LIGE-MEDIATED ALLERGIC DISEASES;
; TILE REFERENCE: UG67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; SOUTHWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8: 177
; MUMBER FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE FERENCE
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (6.17) 742-4214
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acid
TYPE: amino acid
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Xu, H.

ITTLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR PELICATION NUMBER: 60/202
FRIOR PELICATION NUMBER: 60/206,848
FRIOR PELICATION NUMBER: 60/206,848
FRIOR PELICATION NUMBER: 60/206,246
FRIOR APPLICATION NUMBER: 60/206,335
FRIOR APPLICATION NUMBER: 60/230,335
FRIOR FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-09-09
FRIOR PILING DATE: 2000-11-23
FRIOR PELICATION NUMBER: 60/24,578
FRIOR PELICATION NUMBER: 60/25,625
FRIOR PELICATION NUMBER: 60/25,625
FRIOR PELICATION NUMBER: 60/25,636
FRIOR PELICATION NUMBER: 60/25,931
FRIOR PELICATION NUMBER: 60/25,931
FRIOR PELICATION NUMBER: 60/25,930
FRIOR PELICATION NUMBER: 60/25,930
FRIOR PELICATION NUMBER: 60/25,930
FRIOR PELICATION NUMBER: 60/26,308
FRIOR FILING DATE: 2001-02-09
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FRIOR FILING DATE: 2001-02-03
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FRIOR FILING DATE: 2001-02-03
FRIOR FILING DATE: 2001-02-03
FRIOR FILING DATE: 2001-03-0
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1 MMKLLLIAAAAFVAVSADPIHYDKITEEINKAVDEAVAAIEKSETFDPMKVPDHSDKFER
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Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Walone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: For APPLICANT: Xu, TITLE OF INVENT
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Publication No. US:0020168373A1
GENERAL INFORMATION:
APPLICANT: WANTEN R. Thomas and Kaw-Yan Chua
TITLE OF INVENTION: Allergenic Proceins and Peptides From
House Dust Mite and Uses Therefor
                         Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.1%; Score 962; DB 13; Length 215;
85.9%; Pred. No. 3.6e-91;
tive 18; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTER DATE OF THE COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/10/024,955
FILING DATE: 19-06-2001
PRIOR APPLICATION NUMBER: US/08/55,336A
PPLICATION NUMBER: US/08/55,336A
PPLICATION NUMBER: US/08/55,336A
PPLICATION NUMBER: US/08/55,336A
PRILING DATE: 22-UNE-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: M: CAPACITY REGISTRATION NUMBER: M: CAPACITY CONTENT NEORMATION:
TELEPHONE: (617)/42-4214
INFORMATION FOR SEQ ID NO: 2:
                                                                                       12; Indels
                      90.1%; Score 962; DB 10;
85.9%; Pred. No. 3.6e-91;
ive 18; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLSDVLTAIFODTVRKEMTKVLAPAFKRELEKN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-10-024-955-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 15
                   Query Match
Best Local Similarity 85.9
Matches 183; Conservative
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Best Local Similarity 85.95
Matches 183; Conservative
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GENERAL INCRAMICALION
APPLICANT: GELERACH, VALERIE L.
APPLICANT: GELERACH, VALERIE
APPLICANT: GELERACH, VALERIE
APPLICANT: BLIERANN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MATHROON, GLENUDA
TITLE OF INVENTION: MATHROON, GLENUDA
TITLE OF INVENTION: MATHROON GOT USON
TITLE OF INVENTION: MATHROON GOT USON
TITLE OF INVENTION: MATHROON GOT USON
TITLE OF INVENTION NUMBER: GO/190, 645
PRIOR APPLICATION NUMBER: GO/190, 645
PRIOR PLILING DATE: 2000-04-19
PRIOR FILING DATE: 2000-04-26
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                                                            114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEG----NITMTSFEVRQFANVVNHI 169
                                                                                                    162 CKTFILRQLEVAGKEMSEEDVNDMLHQGKWEVFNESLLTEINITKAQLSEIEQRHKELVN 221
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9.0%; Score 96; DB 9; Length 294;
Best Local Similarity 23.8%; Pred. No. 0.23;
Matches 44; Conservative 31; Mismatches 58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
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268 FGLAV 272
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APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: MACDOUGALL, JOHN R.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: METHODS OF USING THE SAME
FILE REFERENCE: 1266-776CIP
CURRENT APPLICATION NUMBER: US/09/898,570
CURRENT FILING DATE: 2001-07-03
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                                                                                                                                                                                                            138 LGDPYPVSSAHGIGTGDVLDAIVDNLPTEAQEE-----SSDIIKFSLIGRPNVGKSSLI 191
                                                                                          ----- 166
                                              ---SMEYDL-AYK 121
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                                                                                                                                                                       122 LGDLHP--TTHVI--SDIODFVV-ALSLEISDEGNITMTSFEVROF
                                                                                                                                                                                                                                                                                                                                                           192 NAILGEDRVIASPVAGTTRDAIDTTFTDEEGQEFTMI 228
                                                                                                                                                                                                                                                                                               167 NHIGGLS--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
                                                  90 AN-----VKGEEGIVK-----AHLLIGVHDDIV---
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PRIOR PILING DATE: 2001-07-03
PRIOR PELING DATE: 2000-04-19
PRIOR PELING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/198,645
PRIOR PILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/199,476
PRIOR PILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR FILING DATE: 2000-04-26
PRIOR PILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 60/204,610
PRIOR APPLICATION NUMBER: 60/20,024
PRIOR PILING DATE: 2000-04-26
PRIOR PELING DATE: 2000-04-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/09898570
Patent No. US2002013312A1
GENERAL INFORMATION:
APPLICANT: GERLACH, VALERIE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
OTHER INFORMATION: Description of
; OTHER INFORMATION: h_nh0778p17_A
US-09-898-570-28
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ORGANISM: Unknown Organism
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PRIOR PERIOR APPLICATION NUMBER: 60/204.9

PRIOR FILING DATE: 2000-04-26

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OTHER INFORMATION: Description of Unknown Organism: POLYX
OTHER INFORMATION: h_nh0778p17_A
US-09-839-446-28
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ORGANISM: Unknown Organism
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Matches 44; Conserva
                170 GGLSI 174
                                                                                         268 FGLAV 272
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FGLAV 272
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US-09-839-446-28
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US-09-839-446-30
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APPLICANT: MACDOUGALL, JOHN N.
APPLICANT: SMITSSON, GLENNUA
ITILE OF INVENTION: MOYEL HUMAN PROTEINS, POLYNUCLECTIDES ENCODING THEM AND
ITILE OF INVENTION: NOVEL HUMAN PROTEINS,
ITILE OF INVENTION: NOVEL HUMAN PROTEINS,
CURRENT PILING DATE: 2001-07-03
FRICK PELICATION NUMBER: US/9/989,570
CURRENT APPLICATION NUMBER: 60/198,645
FRICK PILING DATE: 2000-04-19
FRICK PILING DATE: 2000-04-20
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71 ---LAMRNIEARG------LKOMKROGDANVKGEE-----GIVKAHL--LIGVHDDIVS 113
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COTHER INFORMATION: Description of Unknown Organism: POLYX
COTHER INFORMATION: CG55655_02
CG-09-898-570-32
                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09898570 Patent No. US20020123612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLERMAN, KAREN
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ORGANISM: Unknown Organism
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268 FGLAV 272
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222 LE-----
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND TITLE OF INVENTION: METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown Organism
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                                                                                                               GENERAL INFORMATION:
APPLICANT: ELLERMAN, KAREN
APPLICANT: ELLERMAN, KAREN
APPLICANT: SMACDOUGAAL, JOHN R.
APPLICANT: SMACDOUGAAL, JOHN R.
APPLICANT: SMACDOUGAAL, JOHN R.
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APPLICANT: SMACDOUGAAL, JOHN R.
APPLICANT: SMACDOUGAAL, JOHN R.
APPLICANT: SMACDOUGAAL, JOHN R.
APPLICANTON: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: MCMER: US 001-04-19
CURRENT APPLICATION NUMBER: US 001-04-19
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-26
PRIOR PLING DATE: 2000-04-26
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                       Sequence 30, Application US/09839446 Publication No. US20030050232A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Unknown Organism
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Sequence 32, Application US/09839446
Publication No. US20030050232A1
GENERAL INFORMATION:
APPLICANT: GERLACH, VALERIE I.
APPLICANT: ELLERMAN, KAREN
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA

RESULT 11 US-09-839-446-32

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71 ---LAMRNIBARG------LKOMKRQGDANVKGEE-----GIVKAHL--LIGVHDDIVS 113
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9.0%; Score 96; DB 10; Length 294;
Best Local Similarity 23.8%; Pred. No. 0.23;
Matches 44; Conservative 31; Mismatches 58; Indels
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OTHER INFORMATION: Description of Unknown Organism: POLYX
OTHER INFORMATION: CG55655_02
TILLE OF LINGWILD. METHOLS OF USING IND SAME THE REPRENCE: 15966-776
CURRENT PILING DATE: 2001-04-19
PRIOR PELLORITON NUMBER: 06/198,293
PRIOR PELLORITON NUMBER: 60/198,293
PRIOR PELLORITON NUMBER: 60/198,645
PRIOR APPLICATION NUMBER: 60/198,645
PRIOR APPLICATION NUMBER: 60/210,809
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/200,025
PRIOR FILING DATE: 2000-04-26
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PRIOR PELING DATE: 2000-07-17
PRIOR FILING DATE: 2001-02-27
PRIOR FILING DATE: 2001-02-27
PRIOR FILING DATE: 2011-02-27
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Publication No. US20030215803A1
GENERAL INPORMATION:
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Garcia, Pablo Beninguez
APPLICANT: Scott, Beth
APPLICANT: Scott, Beth
APPLICANT: Cramanac, Radoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
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Leshkowitz, Dena
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170 GGLSI 174
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## APPLICANT: Kita, David
## APPLICANT: Garcia, Veronica
## APPLICANT: Garcia, Veronica
## APPLICANT: Garcia, Veronica
## APPLICANT: Stache-Crain, Birgit
## APPLICANT: Stache-Crain, Birgit
## APPLICANT: Stache-Crain, Birgit
## APPLICANT: Stache-Crain, Birgit
## APPLICANT: Stache-Crain, Birgit
## TITLE OF INVENTION: HUMAN GENE EXPRESSION PRODUCTS
## TITLE OF INVENTION: 1800ATED FROM HUMAN PROSTATE
## TITLE OF INVENTION: 1800ATED FROM HUMAN PROSTATE
## TITLE OF INVENTION: 2001-21
## PRIOR APPLICATION NUMBER: 60/254,648
## PRIOR APPLICATION NUMBER: 60/275,668
## PRIOR APPLICATION NUMBER: 60/275,668
## NUMBER OF SEQ ID NOS: 1568
## SOFWWARE: FastSEQ for Windows Version 4.0
## SEQ ID NOS: 1568
## SOFWWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.0%; Score 96; DB 15; Length 294; Best Local Similarity 23.8%; Pred. No. 0.23; Matches 44; Conservative 31; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 411, Application US/10220120; Publication No. US20040048253A1; GENERAL INFORMATION:
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RUSSO, Frank D.
STOCKDREHER, Theresa K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHEN. Alice
D'SA, Steven A.
AWSHEY, Stefan
DAHL, Christopher R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAHL, Christopher R.
DANIELS, Susan E.
DANIELS, Susan E.
DUFOUR, Gerard E.
FLORES, Vincent
FONG, Willy T.
GREENAWALT, Lila B.
HILLMAN, Jennifer L.
JONES, Anissa L.
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SPIRO, Peter A.
BANVILLE, Steven C.
SHAH, Purvi
CHALUP, Michael S.
CHANG, Simon C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IU, Tommy F.
OSEBERRY, Ann M.
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WRIGHT, Rachel J.
                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-697-1496
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268 FGLAV 272
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CONCENT FILLING APPLICATION NUMBER: 60/184,777; 60/184,779; 60/184,698; 60/184,770; 60/184,774; 60/184,775; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/184,776; 60/186,213; 60/186,213; 60/204,883; 60/205,221; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205,286; 60/205
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OTHER INFORMATION: Incyte ID No. US20040048253A1 LG:204626.1.orf1:2000MAY19
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                                                                                                                                                                        APPLICANT: CHEN, Wensheng
APPLICANT: CCHEN, Howard J.
APPLICANT: CCHEN, Howard J.
APPLICANT: HOUGSON, David M.
APPLICANT: LINCOLN, Stephen E.
APPLICANT: JACKSON, Stuart
TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PT-1113 PCT
CURRENT APPLICATION NUMBER: US/10/220,120
CURRENT FILING DATE: 2002-08-26
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9.0%; Score 96; DB 12; Length 314;
Best Local Similarity 23.8%; Pred. No. 0.25;
Matches 44; Conservative 31; Mismatches 58; Indels
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Publication No. US20040142331A1
GENERAL INFORMATION:
APPLICANT: Jackson, Stuart E.; Lincoln, Stephen E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Ones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Widght, Rachel J.; Gietzen, Darryl;
APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
Jimmy x.
AnLEY, Diana L.
                                                                                                                               BRATCHER, Shawn R. CHEN, Wensheng COHEN, Howard J.
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ORGANISM: Homo sapiens
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Conservative
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
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Best Local Similarity
Matches 47; Conserv
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US-10-282-122A-54874
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 MEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEG----NITMTSFEVRQFANVVNHI 169
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APPLICANT: Gerstin, Ur., Edward H.; Peralta, Careyna H.;
APPLICANT: David, Marie H.; Panzer, Scott R.;
APPLICANT: Forces, Vincent Z.; Daffo, Abel;
APPLICANT: Marwaha, Rakesh, Chen, Alice J.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Inman, Rebekah R.
TITLE OF INVENTION: Molecules FOR DISEASE DETECTION AND TREATMENT FILE REFERENCE: PT-1183 USN
CURRENT APPLICATION NUMBER: 0201-09-05
PRIOR PILING DATE: 2001-09-05
PRIOR PILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,749
PRIOR PILING DATE: 2000-09-05
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PRIOR PILING DATE: 200
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US-10-363-829-449
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9.0%; Score 96; DB 16; Length 31
Best Local Similarity 23.8%; Pred. No. 0.25;
Matches 44; Conservative 31; Mismatches 58; Indels
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ORGANISM: Homo sapiens
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AFFLIGATI'S AU, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR PILING DATE: 2000-03-21
FRIOR FILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-23
FRIOR PILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-26
FRIOR FILING DATE: 2000-05-36
FRIOR FILING DATE: 2000-05-9
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
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FRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 LRFLRLSEVA------EKLOKQAAISIQKGQENYAREMLFQRKKVJQALDKSKRR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MKFLLIAAVAFVAVSADPIHYDKITEBINKAIDDAIAAIEQSBTIDPMKVPDHADKFERH 61
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-64-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 241872 LENGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.9%; Score 95; 20.7%; Pred. No.
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211 QIVELDNPYILLHDKKISSVRDLLTVLDAVAKESKPILLIVAEEVBGEALATLVVANIRGI 270
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Best Local Similarity 22.8%; Pred. No. 2.1;
Matches 54; Conservative 43; Mismatches
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                                                                                                                                                                                                      Sequence 17524, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , TYPE: PRT
, ORGANISM: Xylella fastidiosa
US-10-369-493-17524
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Zyskind, Judith
Wall, Daniel
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Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Grant
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APPLICANT:
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Fublication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Salater, Seeven C.
APPLICANT: Stater, Seeven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B1 US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-22
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                     1170 FKGIQKNKRILVVCDEMTGMEEBHLIPLTKHLIVQRGDSVIKGQQLTDGLVVPHEILEIC 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKGELAMRNI----EARGLKQ-----MKRQGDANVKGE---EGIVKAHLLI--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVHD--DIVSMEYDLAYKLGDLHPTTHVISDIQDFVVAL----SLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 FEVROFANVVN------HIGG-----LSILDPIRGVLSDVLTAIFQDTVR 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 SIGNIIAEAMKKVGKEGVIII--EEGTTLENEL---DVVEGMQFDRGYSSPYFINNQQS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ---KLGDLHPTTH--VISDIQDFVVALSLEISDEGNITMISFEVRQFA---NVVNHIGGL 172
                                                                                                                                                                                                                                                                                                 -----MKVPDHADKFERHVĞIVD
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                                     Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SCHTARE: PatentIn version 3.1
SEQ ID NO 54874
LENGTH: 1397
                                                                                                                                                                                                                                                           66
                                                                                                                                                                                                                        Length 1397;
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                                                                                                                                                                                                                                                     63; Indels
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8.6%; Score 91.5; DB 12;
Best Local Similarity 21.2%; Pred. No. 6.2;
Matches 53; Conservative 35; Mismatches 63;
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8.5%; Score 90.5; DB 15;
Best Local Similarity 22.8%; Pred. No. 2;
Matches 54; Conservative 43; Mismatches 87;
APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                        ; ORGANISM: Chlamydia pneumoniae
US-10-282-122A-54874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Xylella fastidiosa
US-10-369-493-9287
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US-10-369-493-9287
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ORGANISM:
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Serven C.
APPLICANT: Slater, Serven C.
APPLICANT: Slater, Serven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPERSEION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REPERENCE: 38-10[52052]8
FILE REPERENCE: 38-10[52052]8
CURRENT PELLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR PELLOATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

ERNGTH: 547
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173 ----SILDPIFG-----VLSDVL-----TAIFQD---TVRKEMTKVLAPPAFKRELEK 212
                                       :: | | | : | | | :: 327
271 IKVCAVKAPGFGDRRKAMLEDMAVLTGGTVISEEVGLSLEKATTSHLGKAKKVRVSK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 ----SILDPIFG-----VLSDVL-----TAIFQD----TVRKEMIKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VAVSADPIHYDKITEEINKAIDDA-IAAIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
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IIILE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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979 FNTVLDKVEETVEISGESLENNE----MDKAFFSEIFDNVKGIQENLLTGMFRSIEFSIV 1034
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                                                                                                                                                                                                                              1084 -----EQNV-YVDVDVPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESDVITVEEIKD 1135
979 FNTVLDKVEETVEISGESLENNE----MDKAFFSEIFDNVKGIQENLLTGMFRSIETSIV 1034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 KOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 LSLEISDEGNITMTSFEV----ROFANVVNHIGGLS----ILDPIFGVLSDVLTA--IFQ 191
                                                                                                                                                                                             191
                                                                              82 KQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVA
                                                                                                                 1035 IQSEEKVDLN----BNVVSSIL-----DNIENMKEGLLNKLENISSTEGVQETVTEHV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 445. Application US/09925298
Sublication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRICR APPLICATION NUMBER: PCT/US00/05881
PRICR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

8.4%; Score 90; DB
Best Local Similarity 23.3%; Pred. No. 13;
Matches 47; Conservative 43; Mismatches
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1136 EPVQKEVEKETVSIIE-EMEEN 1156
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US-09-925-298-445
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Sequence 3, Application US/09742096

Patent No. US20020155441A1

GENERAL INFORATION:
APPLICANT: DRUILHS, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STACE POLYPEPTIDE MOLECULES
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STACE POLYPEPTIDE MOLECULES
TITLE OF INVENTION WHERE: US/09/742,096
CURRENT APPLICATION NUMBER: US 08/973,642

PRIOR APPLICATION NUMBER: US 08/973,642

PRIOR APPLICATION NUMBER: US 08/973,642

PRIOR APPLICATION NUMBER: PSCT/FR96/00894

PRIOR FILING DATE: 1996-06-12

PRIOR PRILING DATE: 1996-06-13

PRIOR APPLICATION NUMBER: PS/07007
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                                           PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-66
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-09
PRIOR FILING DATE: 2000-12-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-06
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
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PRIOR PELING DATE: 2001-02-16
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PRIOR PELING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 AHLLIGVHDDIVSMEYDLAYKLGDLH---PTTHVISDIODFVVALSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%; Score 90; DB 9; Length 1786; 23.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 90.5; DE; Pred. No. 4.5; 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                       2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Burkholderia cepacia
US-10-282-122A-47806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match.

Best Local Similarity 27.1%;
Matches 29; Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 23.3
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: P. falciparum
US-09-742-096-3
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US-09-742-096-3
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APPLICANT: Monahan, John
APPLICANT: Monahan, John
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Pusztai, Lajos
APPLICANT: Pusztai, Lajos
APPLICANT: Melic, Funda
APPLICANT: Melic, Rodon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US 60/299,887
PRIOR PLILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-07-18
PRIOR PLILING DATE: 2001-07-18
PRIOR PLILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/365,501
PRIOR PLILING DATE: 2002-03-05
PRIOR PLILING DATE: 2002-03-05
PRIOR PLILING DATE: 2002-03-05
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Publication No. US20030096267A1
GENERAL INFORMATION
GENERAL INFORMATION:
APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
APPLICANT: Guzman, Usz-Maria
TITLE OF INVENTION: ESSENTIAL BACTERIAL GENES AND THEIR USF
FILE REFERENCE: 06286-088001
CURRENT APPLICATION NUMBER: US/10/190,279
CURRENT FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US/09/393,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
8.3%; Score 88.5; DB 14;
Best Local Similarity 24.6%; Pred. No. 2.6;
Matches 30; Conservative 25; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 DPIHYDKITEEINKAIDDAIAAIEQSETI---
                                                                                                     Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
                                                                                                                                                                                                                        Wang, Youzne..
Xu, Yongyao
Hoersch, Sebastian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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GE 194
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US-10-190-279-2
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                                                                                                                                                                                                                                                                                                                                                                       Indels 17;
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                                                                                                                                                                                                                                                                                                          Length 405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 445. Application US/10102806
| Publication No. US20030054421A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
| TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
| FILE REFERENCE: PAIO3PICI,
| CURRENT APPLICATION NUMBER: US/10/102,806
| PRIOR PILING DATE: 2002-03-22
| PRIOR PILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05881
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1000-03-08
                                                                                                                                                                                                                                                                                                    Query Match
8.3%; Score 88.5; DB 12;
Best Local Similarity 24.6%; Pred. No. 2.2;
Matches 30; Conservative 25; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                         18 DPIHYDKITEEINKAIDDAIAAIEQSETI--
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 846 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 445 LENGTH: 405
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US-10-177-293-140
US-10-177-293-140

Sequence 140, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 24.6
Matches 30; Conservative
                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:
GE 140
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GE 140
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US-10-102-806-445
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LENGIH: 405
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78 IAMEEADVIVEVVSGKEGITDADEYVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
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138 LGEPLPISSVHGIGTGDVLDAIVENLPNEYEEENPDVIKFSLIGRPNVGKSSLINAILGE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 NRIAGERISIVEDVEGVTRDRIYATGEWINRSFSMIDTGG---IDDVDAPFMEQIKHQAE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT AFFLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/2019,078
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2000-02-05
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-02-06
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PRIOR FILING DATE: 2000-02-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ION: Identification of Essential Genes in Microorganisms
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8.2%; Score 88; DB 12;
Best Local Similarity 21.8%; Pred. No. 2.7;
Matches 46; Conservative 34; Mismatches 89;
                                                                                                               198 DRVIASPVAGTTRDAIDTHFTDTDGQEFTMI 228
                                                               173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Esser
FILE REFRENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                           Sequence 74126, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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US-10-282-122A-74126
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 IAMEEADVIVEVVSGKEGITDADEYVARKLYKTHKPVILAVNKVDNPEMRNDIYDFYALG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 LGDLHPTTHV----ISDIQDFVVALSLEISDEGNITMTSFEVRQFANV-----VNHIGGL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 LGEPLPISSVHGIGTGDVLDAIVENLPNEYEEENPDVIKFSLIGRPNVGKSSLINAILGE 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                             30 NKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGD
                                                                                                                                                                                                                                                                                                                                                                                       42; Gaps
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8.2%; Score 88; DB 10; Length 436;
Best Local Similarity 21.8%; Pred. No. 2.7;
Matches 46; Conservative 34; Mismatches 89; Indels '
                                                                                                                                                                                                                                                                                                                             DB 14; Length 393;
                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 88; DB 14; Length 393
Best Local Similarity 21.8%; Pred. No. 2.3;
Matches 46; Conservative 34; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRVIASPVAGTTRDAIDTHFTDTDGQEFTMI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
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APPLICANT: Wells, Jeremy M
APPLICANT: Hanniffy, Sean B
APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
TITLE REFRENCE: PWC/P21122WO
CURRENT FILING DATE: 2001-01-26
CURRENT FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: CB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR PILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
FRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SEQ ID NO 68
LENGTH: 436
         PRIOR FILING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: 60/099,578
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 68, Application US/09769744A Publication No. US20030134407A1 GENERAL INFORMATION: APPLICANT: Le Page, Richard WF APPLICANT: Wells, Jeremy M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Streptococcus pneumoniae US-09-769-744A-68
                                                                                                                                                                                                                                  ; ORGANISM: Streptococcus pneumoniae
US-10-190-279-2
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DB 12;
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8.2%; Score 88; DB 1

Best Local Similarity 19.4%; Pred. No. 5.5;

Matches 60; Conservative 51; Mismatches
                                                    PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2010-02-09
PRIOR PLING DATE: 2010-02-09
PRIOR PLING DATE: 2010-02-09
PRIOR PLING DATE: 2010-02-06
PRIOR PLING DATE: 2010-02-06
PRIOR PLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-02-16
PRIOR PLING DATE: 2010-03-16
PRIOR PLING DATE: 2010-03-16
PRIOR PLING DATE: 2010-03-16
PRIOR PLING DATE: 2010-03-16
PRIOR PLING DATE: 2001-03-16
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ORGANISM: Staphylococcus haemolyticus
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
LOCATION: (711)...(711)
CTHER INFORMATION: X=any amino acid
US-10-282-122A-71455
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                                                                                                                                                                                                                                                                              APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTIOE ESSENTIAL BACTERIAL GENES AND THEIR USE
FILE REFERENCE: 06286-088001
CURRENT APPLICATION NUMBER: US/10/190,279
CURRENT APPLICATION NUMBER: US/09/393,858
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FRSISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.2%; Score 88; DB 14; Length 436; Best Local Similarity 21.8%; Pred. No. 2.7; Matches 46; Conservative 34; Mismatches 89; Indels
                                              198 DRVIASPVAGTTRDAIDTHFTDTDGQEFTMI 228
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173 S--ILDPIFGVLSDVLTAIFQDTVRKEMTKV 201
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THIE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/191,078
FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Streptococcus pneumoniae US-10-190-279-5
                                                                                                                                                                                              Sequence 5, Application US/10190279
Publication No. US20030096267A1
GENERAL INFORMATION:
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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Forsyth, R.
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 ---DKKVKEVIIATDAGREGELVARLILDKVHNKKPIKRLMISSVTKKAIQEGFKKLKDG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 DHADKFERHVGI----VDFKGELAMRNI--EARGLKQMKRQGDANVKG---EEGIVK---- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 -------AHLLIGVH-DDIVSMEYDLAYKIGDLH-PTTHVIS----DIQDFV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 VALSLEISDE-GNIT------MISFEVROFANVVNHIGG------LSILDPIF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AKKYYTLŚTEIGGLTFQLSTNKQHMTKEDATQIANEIKHVEGNVDSVEKKVKKSHPKPLY 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 GVL----SDVLTAIFQDTVRKEMTKVL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Indels 104; Gaps
- See File Wrapper or PALM.
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: 00/202

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/200,335

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-10-23

PRIOR PLILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

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PRIOR FILING DATE: 2001-02-09

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                                                                                                                                                                          8.1%; Score 87; DB 12; Length 436;
llarity 22.2%; Pred. No. 3.4;
Conservative 41; Mismatches 80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77547, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 ----DAN-----VKGEEGIVKAH----
                                                                        ) ORGANISM: Streptococcus pyogenes US-10-282-122A-74394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Tawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamamcto, Robert
APPLICANT: Frayick, R.
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Best Local Similarity
Matches 47; Conserv
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       LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 TEEINKAIDDAIAAIEQSET--ID-PMKVPDHADKFERHVGIVDFKGELAMRNIEARGLK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERNCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 OMKROGDANVKGEEGIVKAHLL--IGVHDDIVSMEYDLAYKLGD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.2%; Score 87.5; DB 15;
Best Local Similarity 27.8%; Pred. No. 16;
Matches 40; Conservative 19; Mismatches 62;
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 1361
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2006-03-21
PRIOR PELICATION NUMBER: 60/191, 078
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/20, 335
PRIOR APPLICATION NUMBER: 60/20, 335
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/24, 578
PRIOR APPLICATION NUMBER: 60/253, 347
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PELING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-05
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olysen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-369-493-3209
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Yamamoto, Robert
Forsyth, R.
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Sequence 7810, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12179
                                                                                                                                                                                                                                                     Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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US-10-369-493-7810
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                                                                                                                                                                                                                                                                             52 PDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDA-----NVKGEEGIVKAHLLI 105
                                                                                                                                                                                                                                                                                                          6 LIAAVAFVAVSA-------DPIHYDKITEEINKAIDDAIAAIEQSETIDPMKV 51
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                                                                          Query Match 8.1%; Score 86.5; DB 12; Length 544; Best Local Similarity 24.4%; Pred. No. 5.3; Matches 41; Conservative 21; Mismatches 69; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                          106 GVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNIT 153
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APPLICANT: Trawick, John D.
APPLICANT: Carri, Grant J.
APPLICANT: Carri, Grant T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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larity 22.2%; Pred. No. 7;
Conservative 31; Mismatches 50;
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PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-110-27

PRIOR PILING DATE: 2000-112-27

PRIOR PILING DATE: 2000-12-2

PRIOR PILING DATE: 2000-12-2

PRIOR PILING DATE: 2001-12-2

PRIOR PILING DATE: 2001-12-2

PRIOR PILING DATE: 2001-12-2

PRIOR PILING DATE: 2001-12-3

PRIOR PILING DATE: 2001-12-3

PRIOR PILING DATE: 2001-12-3

PRIOR PILING DATE: 2001-12-3

PRIOR PILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5470
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Patent No. US20020061569A1
GENERAL INFORMATION:
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JS-09-815-242-5470
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
; ORGANISM: Vibrio cholerae
US-10-282-122A-77547
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Best Local Similarity
Matches 36; Conserv
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 IFSLLMIALVSFVAMAMFGNKYETPDVIGKSVKEA----EQIFNKNNLKLGKISRSYSD 410
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| : : | : : | | : | | 470 KIEKVYNNQAPKGYIANQSVTANTEIAIHDSNIKLYESLGIK 511
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APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yan, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
8.1%; Score 86.5; DB 9;
Best Local Similarity 22.2%; Pred. No. 7.1;
Matches 36; Conservative 31; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NOS: 14110
SEQ ID NOS: 14110
                                                                                                                                                                                             Sequence 12179, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Query Match
Best Local Similarity 22.0%; Pred. No. 17;
Matches 50; Conservative 35; Mismatches
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CURRENT FILING DATE: 2003-02-0
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/203,335
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
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PRIOR FILING DATE: 2000-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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                                                JS-10-108-260A-2998
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Gcldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
FURENT APPLICATION NUMBER: US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360, 039
PRIOR PRILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                        274 DAAGERATRDVVSRGIYAEMRKSNTSENGGVYISMAHLGPDDVRRRFKGMVKRCADCGFD 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAYKLGDLHPTTH------VISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGDLHPTTHVISDIQDFVVALSLEISDEGNIT--MTSFEVROFANVVNHIGGLSILDPIF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKITEEINKAIDD-----AIAAIEQSETIDPMKV-PDHADKFERHVGIVDFKGELAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 GLSILD-PIF-GVLSDVLTA------IFQDTVRKEMTKVLAPAFKR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 903;
                                                                                                                                                                                                                                                                                             8.1%; Score 86; DB 15; Length 527; llarity 23.5%; Pred. No. 5.7; Conservative 26; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                         66 DFKGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLSPAKEKI -- EAVEKEIDKFLEVINKEELK 766
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FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7810
LENGTH: 527
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; ORGANISM: Methanococcus jannaschii
US-10-369-493-1048
                                                                                                                                                                                                                       ; ORGANISM: Rhodobacter sphaeroides US-10-369-493-7810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.0°
Matches 53; Conservative
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SEQ ID NO 1048
                                                                                                                                                                                                                                                                                                                    1 Similarity
40; Conserv
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Best Local
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68 KGELAM----RNIEARGLKOMKROGDANVKGEEGIVKAH-----LLIGVHDDIVSMEYDLA 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 IHYDKI--TEEINKAIDDAIAAIEQSETIDPMK----VPDHADKFERHV----GIVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1018;
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Sequence 2998, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REPERENCE: HI-AA0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2998
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Sequence 2, Application US/10423483
Publication Wo. US20030226154A1
Publication Wo. US20030226154A1
Publication Wo. US20030226154A1
APPLICANT: Pracek, Louis
APPLICANT: White, H. Steve
APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Ying-Hui
APPLICANT: Skradski, Shana
TITLE OF INVENTION! MASS 1 GENE, A TARGET FOR ANTICONVULSANT DRUG DEVELOPMENT
FILE REPERBNCE: 1321.2.53
CURRENT RILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US/10/220,587
PRIOR FILING DATE: 2002-12-02
               68 KGELAM---RNIEARGLKOMKROGDANVKGEEGIVKAH-----LLIGVHDDIVSMEYDLA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 NGEMILADGRRIVA------NSANVNGRENVVVIHPDFRMIVLANRPGFPFLGNDFF 452
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                                                                                                                                                                   ---IODFVVALS--LEISDEGNITMTS 156
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APPLICANT: Fahy, Eoin D.
APPLICANT: Ehay, Eoin D.
APPLICANT: Ehay, Eoin D.
APPLICANT: Shang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088,465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOPTWARE: FastSEQ for Windows Version 4.0
SOPTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                    157 FEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQ~DTVRKEMTKVL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 824, Application US/10408765A; Publication No. US20040101874A1; GENERAL INFORMATION:
                                                                                                                                                             120 YKLGDLHPTTHVISD-----
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; ORGANISM: Homo sapiens US-10-408-765A-824
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Matches 50; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LSILDP 177
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 55213
LENGTH: 1396
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1. Similarity 23.6%; Pred. No. 26;
49; Conservative 34; Mismatches
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Best Local Similarity 22.0%; Pred. No. 27;
Matches 50; Conservative 35; Mismatches
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Fublication No. US20040038325A1
GENERAL INFORMATION:
APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
APPLICANT: FAGAN, RICHARD JOSEPH
APPLICANT: GTTERINGE, ALEX
TITLE OF INVENTION: ADHESION MOLECTLES
FILE REFERENCE: 674575-2001
CURRENT APPLICATION NUMBER: US/10/346,863
CURRENT PILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: PCT/GB01/03318
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR APPLICATION NUMBER: GB 0018126.3
PRIOR FILING DATE: 2000-07-24
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US-10-282-122A-55213
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US-10-346-863-6
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Best Local Similarity
Matches 49; Conserva
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US-10-346-
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; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-369-493-7986
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                                               : : : : : 2677 NVTYATVPGIVS 2688
                     176 DPIFGVLSDVLT 187
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Best Local Similarity
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                                                                                                                                         US-10-369-493-18437
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US-10-369-493-7986
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APPLICANT: White, H. Steve
APPLICANT: White, H. Steve
APPLICANT: White, H. Steve
APPLICANT: Skradski, Shan
APPLICANT: Skradski, Shan
TITLE OF INVENTION: MASS 1 GENE, A TARGET FOR ANTICONVULSANT DRUG DEVELOPMENT
TITLE OF INVENTION NUMBER: US/10/220,587
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: US 60/187,209
PRIOR FILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Version 3.0
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                                                                                                                                                                                                                                                                                                                              26 TEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHV-----GIVDFKGELAMRNIEA 78
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                                                                                                                                                                                                                                                                                     Indels 41; Gaps
                                                                                                                                                                                                                                               DB 12; Length 2780;
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Best Local Similarity 21.4%; Pred. No. 70;
Matches 41; Conservative 32; Mismatches
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PRIOR APPLICATION NUMBER: US 60/187,209 PRIOR FILING DATE: 2000-03-03 PRIOR PRIOR APPLICATION NUMBER: US 60/222,896 PRIOR FILING DATE: 2000-07-03 NUMBER OF SEQ ID NOS: 33 SOFTWARE: Patentin version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10220587
Publication No. US20030208782A1
GENERAL INFORMATION:
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                                                                                                                                                             TYPE: PRT
CORGANISM: Mus musculus
US-10-423-483-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-10-220-587-2
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Best Local Similarity
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LENGTH: 2780
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: APPLICANT: Cao Vangwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 160426
LENGTH: 281
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                                                                                                                                                                                                             121 KLGDLHPTTHVISD----IQDFVVALSLEISDEGNITWTSFEVROFANVV----NHIGGL 172
                                                                                                                                                                                                                                                                                                                                                     18 DPIH-----YDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA
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7.8%; Score 83.5; DB 12; Length 281;
Best Local Similarity 22.8%; Pred. No. 4.2;
Matches 51; Conservative 36; Mismatches 74; Indels 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_115883C.1.pep
US-10-424-599-160426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRE 209
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| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Sounitra S.
| APPLICANT: Eaby, Eoin D.
| APPLICANT: Zhang, Bing |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Taylor, Steven W. |
| APPLICANT: Glenn, Gary M. |
| APPLICANT: Glenn, Gary M. |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 160426, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-160426
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US-10-408-765A-1398
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APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Walder, Carlos
APPLICANT: Wallos, Carlos
APPLICANT: Carnut Chiese, Receit
APPLICANT: Carr, Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut Carnut 
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                                                                                                                                                                                                                                              68 KGELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHP 127
                                                                                                                                               8 AAVAFVAVSADPIHYDKITEEINKAIDDALAAIEQSETIDPMKVPDHADKFERHVGIVDF 67
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                    67; Gaps
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                    77; Indels
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                    26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71072, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Staphylococcus epidermidis
US-10-282-122A-71072
                        Conservative
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Best Local Similarity
Matches 50; Conserva
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US-10-282-122A-71072
                            47;
                            Matches
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               --NVVNHIGGLSILDPIFGVLSDVLTAIFQDTV 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 MEYDLAYKLGDLHPTTHVISDI-----QDFVVALSLEISDEGNITMTS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERBENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
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Publication No. US20040029129A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          Sequence 3526, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                        341 RKMATLAEAARIKARKEK 358
                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NIZOGUCHI, HIROSHI
APPLICANT: ANDO, SELKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KELKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
                                                                                                          195 RKEMTKVLAPAFKRELEK
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
            149 EGNITMISFEVROFA-
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Wall, Daniel
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Carr, Grant
Yamamoto, Robes
Forsyth, R.
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US-09-738-626-3526
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 168034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SRLTAMKMODEMRIMEEELRDYQRAQDEALTKROLL---EQTLKDLEYELEAKSHLKDDR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 KFERHVGIVDFKGELAMRNIEARGLKOMKROGDANVKGEEG--IVKA-HLLIGVHDDIVS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 HLGKTIEKLQKEMADIVBASRTSTLELQNQLDBYKEKNRRE--LAEMQRQLKEKTLBAEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                      21 HYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKPERHVGIVDFKGELAMRNIEAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 IAAVAFVAVSADPI-----HYDKITEEINKAIDDAIAAIEQ-SETIDPMK-VPDHAD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 83.5; DB 16; Length 405; 24.8%; Pred. No. 7.1; tive 35; Mismatches 82; Indels 77
                                                                                                                                                                                                                                                                                                                           DB 16; Length 360;
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 MEYDLAYKLGDLHPTTHV-------ISDIQDFVVALSLE-----
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT4530_66589C.1.pep
                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6;
; Mismatches
                                                                                                                                                                                                                                                                                                                      1.8%; Score 83.5; ilarity 21.7%; Pred. No. 6; Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168034, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 THVISDIODFVVALSLEISDEGN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 -GLKQMKRQGDANVKGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.8%
....nes 64; Conservative
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                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-408-765A-1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 31
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Sequence 134622 Application US/10437963
; Sequence 134622 Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Mu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 HADKFERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 MEYDLAYKLGDLH---PTTHVISDIQDFVVALSL-EISDEGNITMISFEVRQFANVVNHI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ELAMRNIEARGLKOMKROGDA--NVKG-EEGIVKAHLLIG-VHDDIVSMEYDLAYKLGDL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 HPTTHVISDIQDFVVALSLEISDEGNIT----MISFEVRQFANVVNHIGGLSILDPIFG- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 DP------EDMTSLSAAVENDGEITSDDISTSLPEEEFRDAPSWQEFL--LDGIEGR 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 IHYDKITEEINKAIDDAIAAI------EQSETIDPMKVPDHA--DKFERHVGIVDFKG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 IAAVAF-VAVSADPIHYDKIT-----EEINKAIDDAIAAIEQSETIDPMKVPD
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                                                                                                                                                                                                                                                                                             DB 16; Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.8%; Score 83; DB 16; Length 551; Best Local Similarity 23.1%; Pred. No. 12; Matches 52; Conservative 25; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 GGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAF--KRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 EMDYTAANTTIVD------NVFNIALRYNDTAGTVKVDGKK----
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US-10-437-963-134622
                                                                                                                           FEATURE:
, OTHER INFORMATION: Clone ID: PAT_MRT4530_12903C.1.pep
US-10-437-963-108671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 --VLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 EALLLDDYTLILRN--YKETKRRLA----ELEK 464
                                                                                                                                                                                                                                                                                             7.8%; Score 83.5; D 22.4%; Pred. No. 18; tive 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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Best Local Similarity 22.4%
Matches 48; Conservative
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ORGANISM: Oryza sativa
                                      TYPE: PRT
ORGANISM: Oryza sativa
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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; Sequence 108671, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Buukharov, Andrey A.
; APPLICANT: Brazuk, Brad
; APPLICANT: Brazuk, Brad
; APPLICANT: Brazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TILE REPERENCE: 38-21 (53221)
; FILE REFERENCE: 38-21 (53221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PLING DATE: 2003-05-14
; SEQ ID NO 108671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 AWRNIEARGLKOWKROGDANVKGEEGIVKAHLLIGVHDD---IVSWEYDLAY----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ------SLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 RQFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 -----VNNIMRGIVKVAAVKAPGFG---DRRKAMIQDIATLTAGTVISEEIGLELEK 311
                            CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR PAPLICATION NUMBER: 60/191,078

PRIOR PAPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: 60/269,308

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PRIOR APPLICATION N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , TYPE: PRT
, ORGANISM: Yersinia pestis
US-10-282-122A-78505
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Sequence 14987, Application US/10369493

Sequence 14987, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Gldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 14987

LENGTH: 633
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        --DDVVDADYE 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT , ORGANISM: Agrobacterium tumefaciens US-10-369-493-14213
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603 ----QQAEAGDASAEGK-
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                                                                                                                   Sequence 11797, Application US/10369493

Sequence 11797, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH INPROVED PROPERTIES

FILE REFERENCE: 38-10 (5.052)B

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

NUMBER OF SEQ ID NOS: 47374
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CEDITION NO. US20030233675A1
CEDITION OF US20030233675A1
CEDITION OF US20030233675A1
APPLICANT: Cao, Yongwei
APPLICANT: Goldman, Barry G.
APPLICANT: Goldman, Barry C.
APPLICANT: Coldman, Barry C.
APPLICANT: Coldman, Barry C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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---GKPDPFLFQIKDKLAALYLEGCKAEKGEPLPVGLVDMRELKK 474
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PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14521
LENGTH: 630
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; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11797
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MSJUL 389-566-1559
US-10-389-566-1559
US-10-389-566-1559
Sequence 1559, Application US/10389566
| Publication No. USZO040025202A1
| GENTRAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
| APPLICANT: Monsanto Technology, LLC
| TITLE OF INVENTOR: Nucleic Acid Molecules Associated with Oil in Plants
| FILE REFERENCE: 38-77/52900)
| CURRENT APPLICATION NUMBER: US 60/365,301
| PRIOR PILING DATE: 2002-03-15
| PRIOR FILING DATE: 2002-06-25
| PRIOR FILING DATE: 2002-06-26
| NUMBER OF SEQ ID NOS: 2459
| SOFTWARE: ParentIn Version 3.2
| SEQ ID NO 1559
| LENGTH: 633
   550 DKVSETDRKAIEDAIASLKTAVEAAE-----PDADDIQAKTQTLMEVSMKLGQAIYEA 602
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7.8%; Score 83; DB 16; Length 633;
Best Local Similarity 28.3%; Pred. No. 15;
Matches 28; Conservative 16; Mismatches 27; Indels 2
                                                                           79 RGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
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Patent No. US20020081320A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
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ORGANISM: Leishmania major
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LOCATION: (1)...(845)
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APPLICANT: Gao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Gater, Steven C.
APPLICANT: Gloman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: BEARESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REPERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
FILE REPERENCE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
SRIOR FILING DATE: 2003-02-28
FILE REPERENCE: SEQ ID NOS: 47374
SEQ ID NO 15263
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| Publication No. US20040025202A1 |
| GENERAL INROPARTION: |
| APPLICANT: Monsanto Technology, LLC |
| APPLICANT: Monsanto Technology, LLC |
| APPLICANT: Laurie, Cathy C |
| TITLE OF INVENTION: NUCleic Acid Molecules Associated with Oil in Plants |
| FILE REFRENCE: 38-77(5290)D |
| CURRENT APPLICATION NUMBER: US/10/389,566 |
| CURRENT APPLICATION NUMBER: US 60/365,301 |
| PRIOR FILING DATE: 2002-03-15 |
| PRIOR FILING DATE: 2002-06-25 |
| PRIOR FILING DATE: 2002-06-26 |
| PRIOR FILING DATE: 2002-06-26 |
| NUMBER OF SEQ ID NOS: 2459 |
| SEQ ID NO 1416 |
| LENGTH: 633 |
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Best Local Similarity 28.3%; Pred. No. 15;
Matches 28; Conservative 16; Mismatches 27; Indels 28; Gaps
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79 RGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYD 117
                                                                           603 ----QQAEAGDASAEGK-------DDVVDADYE 624
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15263
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US-10-389-566-1416
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Matches 28; Conservative
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US-10-389-566-1416
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                                                                                                                                                                                                                  89 DANV---KGEEGIVKAHLLIGVHDDIVSNEYDLAYK-LGDLHPTTHVISDIQDFVVALSL 144
                                                                                                                                                                                                                                                53 DKRIMDTRADE-IARG---ITIKSTAISMHYHVPKEMIGDLD-----DDKRDFLINL-- 100
                                                                                                                                                                                                                                                                                                145 BISDEGNITMTSFEVRQFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP 204
                                                                                                                                                                                                                                                                                                                            101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP 151
                                                                                                                                                                29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKOMKRQG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 DANV---KGEEGIVKAHLLIGVHDDIVSMEYDLAYK-LGDLHPTTHVISDIQDFVVALSL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 EISDEGNITMTSFEVRQFANVANHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 -IDSPGHVDFSS-EVTAALRVTD--GALVVVDCVEGVCVQTETVL----RQALTERIRP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 INKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMRNIEARGLKQMKRQG
                                                                                                         34; Gaps
                                                           7.8%; Score 83; DB 9; Length 845; 23.3%; Pred. No. 23; cive 34; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PLOSE, PECET APPLICANT: PLOSE, PECET APPLICANT: Brannon, Mark TITLE OF INVENTION: LEISCHWANIA ANTIGENS FOR USE IN THE TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISCHWANIASIS FILE REFERENCE: 210121.420C9 (CURRENT APPLICATION WOMBER: US/09/991,496 (CURRENT FILING DATE: 2001-11-20 (NUMBER OF SEQ ID NOS: 137 SOFTWARE: PastSEQ for Windows Version 4.0 (ENGTH: 845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.8%; Score 83; DB 9; Length 845; Best Local Similarity 23.3%; Pred. No. 23; Matches 42; Conservative 34; Mismatches 70; Indels
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-874-923-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: 315, 324
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 110, Application US/09991496
Patent No. US20020169285A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
                                          Query Match
Best Local Similarity 23.3*
...hes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Leishmania major
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APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5321)B CURRENT APPLICATION WUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 106024 LENGTH: RS6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13650, Application US/10369493
Sequence 13650, Application US/10369493
Publication No. US2003023367541
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gia, Yorgwei
APPLICANT: Giate, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: GOLDMAN: STRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US 1003-02-28
PRIOR PEDICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 KHRSGKTVF-----ATVKGLKVVFGKGPGSQPIECEDGVYGKSKHTLEARNDLKHIE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 YDLAYKLGDLHPT----THVIS-----DIQDFVVALSLEISDEGNI-TMTSF 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 856;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 EVROFANVVNHIGGLSILDPIFGVLSDVLTAIFODTVRKEMTKV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IAAVAFVAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_10506C.1.pep
US-10-437-963-106024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.7%; Score 82.5; DE
Best Local Similarity 19.6%; Pred. No. 26;
Matches 44; Conservative 48; Mismatches
La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Çao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 63
US-10-369-493-13650
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LENGTH: 1399
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US-10-437-963-106024
; Sequence 106024, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

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APPLICANT: Geriach, Valeite
APPLICANT: Gariach, Valeite
APPLICANT: Gariach, Valeite
APPLICANT: Caterroun, Baida
APPLICANT: Caterroun, Blina
APPLICANT: Leate, Mario W.
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APPLICANT: Leate, Mario W.
APPLICANT: Leate, Mario W.
APPLICANT: Leptey, Denise M.
APPLICANT: Leptey, Denise M.
APPLICANT: Rieger, Catherine E.
APPLICANT: Burgess, Catherine E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 TIDPMKVPDHADKFERHVGIVDFKGEL------AMRNIEARGLKQMKRQG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2498;
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7.7%; Score 82.5; DB 12
Best Local Similarity 24.2%; Pred. No. 1.2e+02;
Matches 39; Conservative 32; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-289-762-894
; Sequence 894, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
Guo, Xiaojia Sasha
Tchernev, Velizar T.
Fernandes, Elma R.
                                                                                                                                                                                                                                  Casman, Stacie J.
Malyankar, Uriel M.
Gerlach, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
US-10-092-900A-218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 244, Application US/10116275
; Sequence 244, Application US/10116275
; Publication No. U220030211476A1
; GENERAL INFORMATION:
; APPLICANT: Bland Pharmaceutical Technology
; APPLICANT: Brayden, David
; APPLICANT: Brayden, David
; APPLICANT: Byrne, David
; APPLICANT: Higgins, Insa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and Methods and
; TITLE OF INVENTION: 2002-10-04
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT PILING DAYE: 2002-10-04
; SEQ ID NOS: 349
; SEQ ID NO 244
indication 3.1
; SEQ ID NO 244
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                                                                                                                                                                                                                                          126 HPTTHVISDIQDFVVALSLEISDEGNITMISFEVRQFANVVNHIGGLSILDPI-FGVLSD 184
                                                                                                                                                                                                                                                                                                686 WSKANDEVSKAM---MANLSKEKVID-----RHGDEVEQE----SFNSMYMMADSGARGS 733
                                                                                                                                          45 TIDPMKVPDHADKFERHVGIVDFKGEL------AMRNIEARGLKOMKROG----- 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 S-----LEISDEGNITMISFEVROFANVVNHIGGLSIL 175
                                                                                       81 ---LKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEY--
                                                                                                                                                                                                                                                                                                     | : | : | 194 GYLTRRLVDVAQDLVVTEIDCGTEHGLLMTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 218, Application US/10092900A Publication No. US20040043382A1 GENERAL INFORMATION:
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Sprek, Kimberly A.
APPLICANT: Tanpier Jr., Raymond J.
APPLICANT: Pena, Carol E.A.
APPLICANT: Li, Li,
APPLICANT: Zerhusen, Bryan D.
APPLICANT: Greev, Vladimir Y.
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                         185 VLTAIFQDIVRKEMTKVLAPA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             843 V---IARDVFKPGTEDVIVPA 860
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Miller, Charles E.
Kekuda, Ramesh
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CRGANISM: Homo sapiens
US-10-116-275-244
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Matches 39; Conserva
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US-10-092-900A-218
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219 NKFTKOGIRILTKA---SISAIEESQNOVRITVNDOVEEFDYVLVAIGROFNTASIGLDN 275
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                385 DGFAAIVSHEITQQILGAYVIGPHASSLIGEMTL----AIRNELT 425
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                                                                                                                                                                                                Sequence 54983, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Cyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yanamoto, Robert
APPLICANT: Yanamoto, Robert
APPLICANT: Porsyth, R.
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US-10-282-122A-54983
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Best Local S
Matches 46
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION WIMBER: US/10/289,762
CURRENT APPLICATION WIMBER: 2003-03-27
SEQ ID NO SEQ ID NOS: 6849
SEQ ID NO 894
LENGTH: 397
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Sequence 399, Application US/09841132
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND FILE REPERENCE: 210121.46698
FILE REPERENCE: 210121.46698
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%; Score 82; DB 15; Length 397; 20.4%; Pred. No. 9.9; Live 44; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 -- FANVVNH-----IGGLSILDPIFGVLSDVLTAIFQDTVRKEMT 199
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b; Pred. No. 12;
44; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                            TYPE: PRT / Chlamydia pneumoniae US-10-289-762-894
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Best Local Similarity 20.4%
Matches 46; Conservative
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Best Local Similarity
Matches 46; Conserv
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: (0/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PLLING DATE: 2000-03-23
PRIOR PLLING DATE: 2000-05-23
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-66
PRIOR PLLING DATE: 2000-05-69
PRIOR PLLING DATE: 2000-01-23
PRIOR PLLING DATE: 2000-01-23
PRIOR PLLING DATE: 2000-11-27
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PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR PLLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PLLING DATE: 2000-12-22
PRIOR PLLING DATE: 2000-12-22
PRIOR PLLING DATE: 2001-10-2-9
PRIOR PLLING DATE: 2001-10-2-9
PRIOR PLLING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MKFLLIAAVAFVAVSADP----IHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Gaps
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FOURILICATION NO. US20030073094A1
GENERAL INFORMATION:
TATLE OF INVENTION: Stress Proteins and Uses Therefor NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
DIRECT: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.6%; Score 81.5; DB 12; Length 445; Best Local Similarity 24.2%; Pred. No. 13; Matches 47; Conservative 26; Mismatches 70; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 -FANVVNHIGGLSI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GIVDFK-GELAMRN---IEARGL--KOMKROGDANVKGEEGIVKAHL--LIGVHDDI--V 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 NTLDIEYGDQMVTSDYMIQLRDLLYKVMTQGGNANLTALSIFMESHIEAFISVLDQIKQT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IAAVAFVAVSADPI--HYDKITE-EINKAIDDAIAAIEQSETIDPMKVPDH-ADKFERHV
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7.7%; Score 82; DB 9; Length 785;
Best Local Similarity 23.6%; Pred. No. 26;
Matches 63; Conservative 38; Mismatches 80; Indels
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: NAXAGARA, SATOSHI
APPLICANT: MAZOGUCHI, HIROSHI
APPLICANT: ANDO, SELKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: CCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TEKEDA, MASATO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OZAKI, AKIO
TITE OF INVERTION: NOWEL POLYMUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 DPIFGVLSDVLTA-IFQDTVRKEMTKV 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Gaps

17;

Length 745; Indels

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77 EARGLKQMKRQGDANVKGEEGIVKAHLL----IGVHDDIVSMEYDLAYKLGDLHFTTHVI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
FUREBRY APPLICATION NUMBER: 105/10/282,122A
CURRENT APPLICATION DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application data removed - See File Wrapper or PALM.
                                                                                                                                                                                                                                                                                                                                                        DB 15;
                                                                                                                                                                                                                                                                                                                                                    Query Match 7.6%; Score 81.5; Di
Best Local Similarity 25.2%; Pred. No. 27;
Matches 30; Conservative 26; Mismatches
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 2657
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-202-122A-52455
; Sequence 52455, Application US/10282122A
; Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/20,335
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
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PRIOR PELING DATE: 2001-02-16
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ORGANISM: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Halone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Synechocystis sp.
US-10-369-493-2657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
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SEQ ID NO 52455
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFIBINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 PETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATA----
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                                                          MEDIUM TITES: FIOPY GISE

COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/046,649
FILING DATE: 14-Jan-2002
CLASS:FICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 08/073,381
FILING DATE: 09-DEC-1991
APPLICATION NUMBER: US 07/804,632
FILING DATE: 15-JUN-1989
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1989
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1989
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1989
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%; Score 81.5; Di
20.4%; Pred. No. 18;
tive 37; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 PTTHVISDIQDFVVALSLEISD-----
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Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 861-6240 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 547 amino acids
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    COMPUTER READABLE FORM:
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Matches 48; Conserva
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DB 12; Length 1279;

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117 --DLAYKIGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIG---- 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 VKAHLL--IGVHDDIVSMEYDL--------AYKLGDLHPTTHVISDI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 ODFVVALSLEISDEGNITMISF-----EVROFANVVNHIGGLSILDPIFGVLS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MKFLLIAAVAFVAVSA-DPIHYDKITEEINKA--IDDAIAAIEQSETIDPMKVPDHADKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 EQSETIDPMKVPDHADKF--ERHVGIVDFKGELAMRNIEARGLKQMKRQGDANVKGEEGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 296;
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Publication No. US2003004009141
GENERAL INFORMATION:
APPLICANT: Trimbur, Donald E.
APPLICANT: Trimbur, Donald E.
APPLICANT: Selifonova, Olga V.
TITLE OF INVENTION: Mutear I. 3-Propanediol Dehydrogenase
FILE REFERENCE: GC580-2D1
CURRENT APPLICATION NUMBER: US/09/991,138
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: US 09/570,778
PRIOR APPLICATION NUMBER: US 09/570,778
PRIOR APPLICATION NUMBER: US 60/134,868
PRIOR PILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Indels
                                                                                                                                                                                 FEATURE:

NAME/KEY: Unsure

LOCATION: (1). (296)

OTHER INFORMATION: unsure at all Xaa locations
FEATURE:

PEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_58074C.1.pep
US-10-424-599-239257
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7.6%; Score 81; DB 12;
Best Local Similarity 21.6%; Pred. No. 8.3;
Matches 44; Conservative 37; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ----DVLTAIFQDTVRKEMTKVL 202
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; ORGANISM: Clostridium pasteurianum
US-09-991-138-12
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                          NUMBER OF SEQ ID
SEQ ID NO 239257
LENGTH: 296
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Publication No. US20040031072A1

GENERAL INFORMATION:
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                                                                                                                           75 ----NIEARGLKOMKROGDANVKGEEGIVKAHLLIGV-----HDDIVSMEYDLAYKL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 AMRNIEARGLK---QMKRQGDANVKGEEGIVKAHLLIGV---HDDIVSMEYDLAYKLGDL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --HPTTHVISDI----QDFVVALSLEISDEGNITMTSFEVRQFA--NVVNHIGGLSILDP 177
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                                                                                             23 DKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELAMR----
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                       123 GDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQFANVVNHIGGLSILD 176
                                    61;
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                                    47; Indels
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Best Local Similarity 23.0%; Pred. No. 60; Matches 40; Conservative 26; Mismatches
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ORGANISM: Glycine max
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SEQ ID NO 48944
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANT: Chen, Xianfeng
APPLICANTON: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: 28-10(5.06.2)8
TITLE REPREBUCE: 38-10(5.06.2)8
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-28
PRIOR PELING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 VHAWAHQLGGLYDMAHGVAN-----AMLLPHVERYNLISNP---KKFADIAEFMGENIE 314
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA-014A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Ralnow, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Publication No. US20030233675A1
                                                                                     171 GLSI-----LDPIFGVLSDV 185
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
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73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLGDLHPTTH-- 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
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212 ECEMEKPYILIYDKKISNLKDFLPILEPAVQ----
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7.6%; Score 81; DB 1
Best Local Similarity 20.3%; Pred. No. 20;
Matches 43; Conservative 33; Mismatches
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APPLICANT: Ld., Preeti
APPLICANT: Ld., Preeti
APPLICANT: Ld., Preeti
APPLICANT: BAINGAN, Chandra
APPLICANT: BAINGAN, Olga
APPLICANT: AZIXZAI, Yalda
APPLICANT: TANG, Y. TOM
APPLICANT: TANG, Y. TOM
APPLICANT: SHAH, Purvi
APPLICANT: SHAH, Purvi
APPLICANT: REDDY, Roopa
TITLE OF INVENTION: TANSCRIPTION FACTORS
FILE REFERENCE: PF-0761 PCT
CURRENT APPLICATION NUMBER: US/10/221, 625
CURRENT APPLICATION NOWSER: US/10/221, 625
CURRENT FILING DATE: 201-03-13
NUMBER OF SEQ ID NOS: 214
SOFTWARE: PROGRAM
SSEQ ID NOS: 214
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-10-36
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2001-02-09
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                 Query Match
Best Local S:
Matches 41
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CURRENT APPLICATION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: 06/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PRICH APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PRILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 57903
LENGTH: 245
                                                                                                                                                                                                                                              36;
                                                                                                                                                                                     Ouery Match 7.6%; Score 81; DB 12; Length 767; Best Local Similarity 22.9%; Pred. No. 32; Matches 36; Conservative 29; Mismatches 56; Indels
                                                                             NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 1359294CD1
US-10-221-625-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ::|| : :|| | : :|| 652 DQFGFINYEVGDSKKLFFHVKEVQD---GIELQAGDE 685
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    TYPE: PRT
    ORGANISM: Enterococcus faecium
US-10-282-122A-57903

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APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
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Forsyth, R.
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Carr, Grant
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 HPTTHVISDIQDFVVALSLEISDEGNITWISFEVROFAN------VVNHIGGLSIL 175
                                                                                                                                                                            64 IVDFKGEL---AMRNIEARGLKQMKRQGDAN------VKGEEGIVKAHLLI---GVH 108
                                                                                                                                                                                                                                                                                                                                                                  109 DDIVSMEYDLA-YK-----LGDLHPTTHVISDI----QDFVVALSLEISDEGNITMTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                             93 NDKLYMRMDAEDFKKCLDINLIGTFNMTQHVLKKOMKQREGAIINLSSVSGLIGNIGQAN 152
                                                                                                                                                                                                                                            72 AMRNIEARGLK---OMKROGDANVKGEEGIVKAHLLIG---VHDDIVSMEYDLAYKLGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 KAIDDAIA-----AIEQS----ETIDPMKVPDHADKFERHVGIVDFKGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 FEVROFANVVNHIGGLSILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.5%; Score 80.5; DB 12; Length 3
24.6%; Pred. No. 11;
tive 32; Mismatches 60; Indels
                                                                                             69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Clone ID: PAT_MRT3847_202C.1.pep
US-10-424-599-197424
ch 7.5%; Score 80.5; Di
1 Similarity 23.3%; Pred. No. 7.1;
41; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 166336, Application US/10437963; Sequence 16636, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
APPLICANT: Kovalic, David K.; APPLICANT: Zhou, Yihua; APPLICANT: Cao, Yongwei; APPLICANT: Boukharov, Andrey A.; APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 DP----IFGVLSDV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || ::| |: |
179 DPDENAAVYGSLATV 193
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Best Local Similarity 24.64
Matches 48; Conservative
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ORGANISM: Glycine max
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 05/10/282,122A
CURRENT PLING DATE: 2003-02-20
RIOR APPLICATION NUMBER: 60/191,078
RIOR FILING DATE: 2000-03-21
RIOR FILING DATE: 2000-05-23
RIOR APPLICATION NUMBER: 60/207,727
RIOR FILING DATE: 2000-05-26
RIOR FILING DATE: 2000-05-26
RIOR FILING DATE: 2000-05-26
RIOR FILING DATE: 2000-09-06
RIOR APPLICATION NUMBER: 60/230,347
RIOR FILING DATE: 2000-09-09
RIOR FILING DATE: 2000-01-02
RIOR FILING DATE: 2000-10-23
RIOR FILING DATE: 2000-11-27
RIOR FILING DATE: 2000-11-27
RIOR FILING DATE: 2000-11-27
RIOR FILING DATE: 2000-11-22
RIOR FILING DATE: 2000-11-22
RIOR FILING DATE: 2000-11-22
RIOR FILING DATE: 2000-11-22
RIOR FILING DATE: 2000-11-22
RIOR FILING DATE: 2001-02-09
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RIOR FILING DATE: 2001-02-09
RIOR FILING DATE: 2001-02-09
RIOR FILING DATE: 2001-02-09
RIOR FILING DATE: 2001-02-09
                 120
                                                                                                                                                                                          208 PEAGSIELENPYILLVDKKISNIRELLPVLEGVAKASKPLVIIAEDVEGEALATL---- 262
                                                -----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 ROFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
                                                                                                                                                                                                                                                                                                            263 ----VVNNWRGIVKVAAVRAPGFG---DRRKAMLQDIATLTNGTVISEEIGLELEK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 VAVSADPIHYDKITEEINKAIDDAIA-AIEQSETIDPMKVPDHADKFERHVGIVDFKGEL
          72 AMRNIBARGLKQMKRQGDANVKGBEGIVKAHLLIGVHDD---IVSMBYDLAY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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7.5%; Score 80.5; D
Best Local Similarity 18.1%; Pred. No. 22;
Matches 43; Conservative 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56251, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                      121 -----
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SEQ ID NO 56251
LENGTH: 547
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Publication No. US2030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Stater, Steven C.

APPLICANT: Stater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

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APPLICANT: Green, C.

APPLICANT: Goldman, Barry S.

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                 APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
File Reperence: 38-21 (53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO 166236
SEQ ID NO 166236
LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RQGDANVKGEEGIVKAHLLI----GVHDDIVSMEYDL------AYKLGDLHPT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 TSNHHHQQGNNNRVPDDPYAKVKFKIPSFWGYYDAEKYLNXEMTVEQKFSAHLVPKQHRV 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 -----PMK--VPDHADKFERHVGIVDFKGELAMRNIEARGLKOMK----
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US-10-437-963-166236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.5%; Score 80.5; DB 16; Best Local Similarity 20.3%; Pred. No. 11; Matches 43; Conservative 34; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(324)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 THVISDIODFVVALSLEISDEGNITMTSFEVR 160
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18.6%; Pred. No. 22;
tive 42; Mismatches
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; ORGANISM: Xenorhabdus nematophilus
US-10-369-493-181
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Barbazuk, Brad
                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 44; Conserv
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF EXQ ID NOS: 47374
LENGTH: 720
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                                                                                                                                                                                                            45 TIDPMKVPDHADKFERHVGIVDFKGELAMRNIEAR--GLKQ-MKRQGDANVKGEEGIVKA 101
                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                 129 HLI-----EYKIKHDLPNECPL--IILKFDDMMDGSRWE---EFNLDWTMGCRRQ 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 FANVVNH------IGGLS-----ILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAF 206
                                                                                                                                                                                                                                                                                                                                                             102 HLLIGVHDDIVSMEYDLAYKLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEVRQ
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                                                          7.5%; Score 80; DB 16; Length 600; 25.1%; Pred. No. 29; It; Pred. 24; Mismatches 74; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSC-09-738-626-5468
; Sequence 5468, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORVATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10217, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Cytophaga hutchinsonii
US-10-369-493-10217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 LDPIFGVLSDVLTA 188
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688 LYPFTGFLLNPMIA 701
                                                                                              Best Local Similarity 25.1
Matches 45; Conservative
US-10-437-963-144132
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US-10-369-493-10217
                                                                      Query Match
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; Sequence 144132, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yihua
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Barbazuk, Brad
    APPLICANT: Barbazuk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(3321)B
    CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-369-493-5550

is Sequence 5550, Application US/10369493

j Sequence 5550, Application US/10369493

j Publication No. US20030233675A1

j APPLICANT: Cao, Yongweir

j APPLICANT: Slater, Steven C.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Marry S.

APPLICANT: Chen, Xianteng

j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

PRIOR FILING DATE: 2002-02-21

j SEQ ID NOS: 47374

j SEQ ID NO 5550

LENGTH: 160
                                                                                                                                             208 PETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLVIIAEDVEGBALATL---- 262
157 TVGKLIAEAMDKV-----GKEGVITVEDGTGLEDELDVVEGMQFDRGYLSPYFINK 207
                                                                      ----KLGDLHPTTHVISDIQDFVVALSLEISDEGNITMTSFEV 159
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                                                                                                                                                                                                                                                                   263 -----VVNTWRGIVKVAAVKAPGFG---DRRKAMLQDIATLTGGTVISEBIGMELEK 311
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OTHER INFORMATION: Clone ID: PAT_MRT4530_44977C.1.pep
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US-10-369-493-5550
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US-10-437-963-144132
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LENGTH: 600
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Best Local S
Matches 27
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183 ----SDVLTAIFQDTVRKEMTKVLAPA-FKR 208
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CORGANISM: Homo sapiens
US-10-093-463-126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 ELAMRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHD--DIVSMEYDLAYKLGDLHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 TTHVISDIQDFVVALSLEISDEGNITWTSFEVROFANVVNHIGGLSILDPIFGVLS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              DB 9; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 INKAIDDAIAAIEQSETIDP---MKVPDHADKFER--
                                                                                                                                                                                                                                                                                                                                                                                                              7.5%; Score 80; DB 9 24.4%; Pred. No. 46; tive 31; Mismatches
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRICE APPLICATION NUMBER: UP 99/377484
PRICE FILING DATE: 1999-12-16
PRICE FILING DATE: 1999-12-16
PRICE FILING DATE: 2000-04-07
PRICE FILING DATE: 2000-04-07
PRICE FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PACENTIN VET: 3.0
SEQ ID NO 5468
LENGTH: 831
                                                      APPLICANT: IKEDA, MASATO
APPLICANT: OZAKT, AKTO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 126, Application US/10093463
Publication No. US20030208039A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Padigaru, Muralidhara APPLICANT: Shenoy, Suresh APPLICANT: Rekuda, Ramesh APPLICANT: Rekuda, Ramesh APPLICANT: Pochart, Pascal APPLICANT: Zhong, Mei APPLICANT: Rastelli, Luca APPLICANT: Rastelli, Luca APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda APPLICANT: Guo, Xiaojia APPLICANT: Guo, Xiaojia APPLICANT: Gasman, Stacie
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Liu, Xiaohong
Spytek, Kimberly
Gorman, Linda
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Gangolli, Esha
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Voss, Edward
Malyankar, Uriel
Anderson, David
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zerhusen, Bryan
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Best Local Similarity
Matches 43; Conserv
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APPLICANT: Patturejan, Meera
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Miller, Charles
APPLICANT: Tupler, Charles
TITLE OF INVENTION: No. US200320803Ae1 Antibodies that bind to Antigenic Polypeptic
TITLE OF INVENTION: No. US200320803Ae1
TITLE OF INVENTION: Encoding The AAttigens, and Methods of Use.
CURRENT PAPLICATION NUMBER: 1202-06-34
PRIOR PLING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-14
PRIOR PLING DATE: 2001-06-16
PRIOR APPLICATION NUMBER: 60/274, 281
PRIOR PLING DATE: 2001-06-16
PRIOR PLING DATE: 2001-06-16
PRIOR PLING DATE: 2001-06-16
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7.5%; Score 80; DB 15;
Best Local Similarity 19.9%; Pred. No. 2.9e+02;
Matches 54; Conservative 43; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 -EYDLAYKLGDLHPTTHVISDIOD---
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42; Mismatches
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17.8%; Pred. No. 28
                                                                     Sequence 73215, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella paratyphi A
                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Forsyth, R.
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Best Local Similarity 17.8
Matches 42; Conservative
                                                                                                                                                                                                                                                                                  Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                            Danie
                                                                                                                                                                                                                                                                                    Trawick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ROFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212
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                                                                                                                                                                                                                                                                                                                                                                                                                            TION: Identification of Essential Genes in Microorganisms
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---LAPAEFER 898
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TITLE OF INVENTION: IGENELA-
FILLE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/191,078
FRIOR FILING DATE: 2000-03-21
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
FRIOR APPLICATION NUMBER: 60/207,727
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17.7%; Pred. No. 14;
Live 46; Mismatches
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                                                                                                                    Sequence 68540, Application US/10282122A
Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-29
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                   LICANT: Wang, Liangsu
LICANT: Zamudio, Carlos
LICANT: Malone, Cheryl
LICANT: Haselbeck, Robert
LICANT: Zyskind, Judith
LICANT: Zyskind, Judith
LICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-10-282-122A-68540
                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert
Forsyth, R.
| | | | | | 875 TAVINADVTIHIFQTT
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Carr, Grant
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Best Local Similarity
Matches 42; Conserv
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PRIOR APPLICATION NUMBER: 60/191, 078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR PLICATION NUMBER: 60/200, 335

PRIOR APPLICATION NUMBER: 60/200, 335

PRIOR APPLICATION NUMBER: 60/200, 335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PELICATION NUMBER: 60/245,578

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-12-20

PRIOR PLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

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PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 13 VAVSADPIHYDKITEEINKAIDDAIAAIEQSETIDPMKVPDHADKFERHVGIVDFKGELA 209 ETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATL-----161 QFANVVNHIGGL----SILDPIFGVLSDVLTAIFQDTVRKEMTKVLAPAFKRELEK 212 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms 73 MRNIEARGLKOMKROGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY---Length 547; Indels DB 12; 85,

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Sequence 76037, Application US/10282122A
Publication No. US20040029129A1
                         Publication No. U220040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Wandne, Carlos
APPLICANT: Wandne, Cheryl
APPLICANT: Hasolbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                             Carr, Grant
Yamamoto, Robert
Forsyth, R.
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ORGANISM: Salmonella typhi
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FORESTA, R.
APPLICANT: FORESTA, R.
APPLICANT: Tandemoulcy, ROUGEL
APPLICANT: TAN, H.
TITLE OF INVARITOR: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: 60/101,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 548;
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                                            Sequence 75259, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Ralno, Carlos
APPLICANT: Malone, Chery1
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin version 3.1
SEQ ID NO 75259
LENGTH: 548
                                                                                                                                                                                                                                                   Zyskind, Julith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity
Matches 42; Conserva
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73 MRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDD---IVSMEYDLAY------ 120
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                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PAPLICATION NUMBER: 60/207,727
PRIOR PAPLICATION NUMBER: 60/230,335
PRIOR PAPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-01-03
PRIOR PILING DATE: 2000-10-23
PRIOR PAPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR PAPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: BLITRA.034A
CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT PILING DATE: 2003-02-20
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RESULT 94 US-10-282-122A-44041 Sequence 44041, Application US/10282122A ; Publication No. US20040029129A1

RESULT 93 US-10-282-122A-76037

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; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10901
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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TITLE OF INVENTION: Identification of Bssential Genes in Microorganisms
FILE REFERENCE: ELITAA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/200

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/203

PRIOR PLING DATE: 2000-03-23

PRIOR PLING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PRIOR APPLICATION NUMBER: 60/25,625

PRIOR PRILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-23

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PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-29

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2010-02-09

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PRIOR PLING DATE: 2010-0
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Udith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus aureus
US-10-282-122A-44041
Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                         Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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LENGTH: 664
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.0348
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yau, H. Howard
APPLICANT: Xu, H. Howard
TTTLE OF INVENTION: Identification of Essential Genes in
TTTLE OF INVENTION: Prokaryotes
FILE REFRENTE ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/207
PRIOR APPLICATION NUMBER: 60/207
PRIOR APPLICATION NUMBER: 60/207
PRIOR APPLICATION NUMBER: 60/207
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 10901
LENGTH: 718
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7.4%; Score 79.5; D. Best Local Similarity 19.9%; Pred. No. 42; Matches 45; Conservative 36; Mismatches
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APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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29skind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Sequence 126, Application US/10369493

Sequence 126, Application No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Chec, Yongwei
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 126

SEQ ID NO 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 SRNRSTSMI--LNDILSQLRYDGSADGIKSLINATREKLSCKRFLVVIDDIASIETWNSI 284
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                                                                                                                                                                                                                                                                                                                                 65 -VDFKGELAMRNIEARGLKQMKRQGDANVKGEEGIVKAHLLIGVHDDIVSMEYDLAYKLG 123
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                                                                                                                                                                                                         : : | | : | | : | : | : | : | 10 PCEVITQLIMEDWEGESVQHPK---VVSIVGFGGLGKTTLASQVYKKIHSRFECAVFVFA
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                                                                                                                                                    19 PIHYDKI-----TEEINKA----IDDAIAAIEQSETIDPMKVPDHADKFERHVGI--
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                                                                   29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1006;
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20.5%; Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 FGVLSDVLTA---IFQDTVRKEMTKVLAPAF 206
                   Best Local Similarity 21.3%; Pred. No. 48;
Matches 45; Conservative 40; Mismatches
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US-10-219-834-150
Sequence 150, Application US/10219834
; Publication No. US20030096751A1
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ORGANISM: Aquifex aeolicus
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Best Local Similarity
Matches 50; Conserv
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884 RIDE
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APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Applicant: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Moi wei
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APPLICANT: Barbazuk, Brad
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PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 6/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-05-06

PRIOR FILING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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PRIOR FILING DATE: 2001-02-04

PRIOR PELING DATE: 2001-02-16

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US-10-437-963-148847
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Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Clostridium difficile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-437-963-148847
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                                                                                                                                                                                                     53; Gaps
                                                                                                                               Query Match 7.4%; Score 79.5; DB 14; Length 1615; Best Local Similarity 20.9%; Pred. No. 1.3e+02; Matches 41; Conservative 32; Mismatches 70; Indels 53;
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Job time : 49 secs
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428 LGAINVTYTTVPGMLS 443
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-149
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              TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE FFILE REFERENCE: DO191 NP

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE FFILE REFERENCE: DO191 NP

CURRENT APPLICATION NUMBER: US (0/313,658

PRIOR APPLICATION NUMBER: US (0/313,658

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-09-12

PRIOR FILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2002-02-06

PRIOR PILING DATE: 2001-09-12

PRIOR PILING DATE: 2001-11-26

PRIOR PILING DATE: 2001-12-06

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Publication No. US20030096751A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE

FILE REFERENCE: D0191 NP

CURRENT APPLICATION NUMBER: US 60/313,658

PRIOR APPLICATION NUMBER: US 60/340,703

PRIOR APPLICATION NUMBER: US 60/340,703

PRIOR PILING DATE: 2001-09-12

PRIOR APPLICATION NUMBER: US 60/318,675

PRIOR FILING DATE: 2001-09-12

PRIOR FILING DATE: 2001-09-12

PRIOR FILING DATE: 2001-09-12

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-26

PRIOR FILING DATE: 2001-11-36

NUMBER OF SEQ ID NOS: 192

SEQ ID NO 149

LENGTH: 1615
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20.9%; Pred. No. 1.38+02;
tive 32; Mismatches 70; Indels
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ORGANISM: Homo sapiens
US-10-219-834-150
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Best Local Similarity
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